

SEQUENCE LISTING

<110> Yale University
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Clyne, Peter J.
Warr, Coral G.

<120> Novel Family of Odorant Receptor Genes in Drosophila

<130> 44574-5061-WO

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<150> US 60/117,132

<151> 1999-01-25

<160> 112

<170> PatentIn Ver. 2.1

<210> 1

<211> 767

<212> DNA

<213> Drosophila melanogaster

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<221> CDS

<222> (1)..(765)

<223> DOR 22A.2, coding region of NCBI Accession No.
AF127924

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cgg gtt aag tcc cga gat gcc ttc gtt tac tta gat cgg gtg atg tgg	96
Arg Val Lys Ser Arg Asp Ala Phe Val Tyr Leu Asp Arg Val Met Trp	
20 25 30	

tcc ttt ggc tgg aca gtg cct gaa aac aaa agg tgg gat cta cat tac	144
Ser Phe Gly Trp Thr Val Pro Glu Asn Lys Arg Trp Asp Leu His Tyr	
35 40 45	

aaa ctg tgg tca act ttc gtg aca ttg ttg ata ttt atc ctt ctg ccg	192
Lys Leu Trp Ser Thr Phe Val Thr Leu Leu Ile Phe Ile Leu Leu Pro	
50 55 60	

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 <213> Drosophila melanogaster

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Ser	Phe	Gly	Trp	Thr	Val	Pro	Glu	Asn	Lys	Arg	Trp	Asp	Leu	His	Tyr	35	40	45	
Lys	Leu	Trp	Ser	Thr	Phe	Val	Thr	Leu	Leu	Ile	Phe	Ile	Leu	Leu	Pro	50	55	60	
Ile	Ser	Val	Ser	Val	Glu	Tyr	Ile	Gln	Arg	Phe	Lys	Thr	Phe	Ser	Ala	65	70	75	80
Gly	Glu	Phe	Leu	Ser	Ser	Ile	Gln	Ile	Gly	Val	Asn	Met	Tyr	Gly	Ser	85	90	95	
Ser	Phe	Lys	Ser	Tyr	Leu	Thr	Met	Met	Gly	Tyr	Lys	Lys	Arg	Gln	Glu	100	105	110	
Ala	Lys	Met	Ser	Leu	Asp	Glu	Leu	Asp	Lys	Arg	Cys	Val	Cys	Asp	Glu	115	120	125	
Glu	Arg	Thr	Ile	Val	His	Arg	His	Val	Ala	Leu	Gly	Asn	Phe	Cys	Tyr	130	135	140	
Ile	Phe	Tyr	His	Ile	Ala	Tyr	Thr	Ser	Phe	Leu	Ile	Ser	Asn	Phe	Leu	145	150	155	160
Ser	Phe	Ile	Met	Lys	Arg	Ile	His	Ala	Trp	Arg	Met	Tyr	Phe	Pro	Tyr	165	170	175	
Val	Asp	Pro	Glu	Lys	Gln	Phe	Tyr	Ile	Ser	Ser	Ile	Ala	Glu	Val	Ile	180	185	190	
Leu	Arg	Gly	Trp	Ala	Val	Phe	Met	Asp	Leu	Cys	Thr	Asp	Val	Cys	Pro	195	200	205	
Leu	Ile	Ser	Met	Val	Ile	Ala	Arg	Cys	His	Ile	Thr	Leu	Leu	Lys	Gln				

210

215

220

Arg Leu Arg Asn Leu Arg Ser Glu Pro Gly Arg Thr Glu Asp Glu Tyr
 225 230 235 240

Leu Lys Glu Leu Ala Asp Cys Val Arg Asp His Arg Leu Ile Leu
 245 250 255

<210> 3

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<212> DNA

<213> Drosophila melanogaster

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<221> CDS

<222> (1)..(1137)

<223> DOR 22C.1, a coding segment on BDGP Clone No.
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ccc cgc atc tcc ggc ctc att gtc ggc ctc tgg ccg caa agg ata agg 96
 Pro Arg Ile Ser Gly Leu Ile Val Gly Leu Trp Pro Gln Arg Ile Arg
 20 25 30

ggc ggg ggc ggt cgt cct tgg cac gcc cat ctg ctc ttc gtg ttc gcc 144
 Gly Gly Gly Gly Arg Pro Trp His Ala His Leu Leu Phe Val Phe Ala
 35 40 45

ttc gcc atg gtg gtg gtg ggt gcg gtg ggc gag gtg tcg tac ggc tgt 192
 Phe Ala Met Val Val Val Gly Ala Val Gly Glu Val Ser Tyr Gly Cys
 50 55 60

gtc cac ctg gac aac ctg gtg gtg gcg ctg gag gcc ttc tgc ccc gga 240
 Val His Leu Asp Asn Leu Val Val Ala Leu Glu Ala Phe Cys Pro Gly
 65 70 75 80

acc acc aag gcg gtc tgc gtt ttg aag ctg tgg gtc ttc ttc cgc tcc 288
 Thr Thr Lys Ala Val Cys Val Leu Lys Leu Trp Val Phe Phe Arg Ser
 85 90 95

aat cgc cgg tgg gcg gag ttg gtc cag cgc ctg cgg gct att ttg ctc 336
 Asn Arg Arg Trp Ala Glu Leu Val Gln Arg Leu Arg Ala Ile Leu Leu

100	105	110	
agc ctg ttg ttg ctc agc tct ggc acg gcg aca aat gcc gcc ttc acc			384
Ser Leu Leu Leu Leu Ser Ser Gly Thr Ala Thr Asn Ala Ala Phe Thr			
115	120	125	
ttg caa ccg ctg att atg ggt ctc tac cgc tgg att gtg cag ctg cca			432
Leu Gln Pro Leu Ile Met Gly Leu Tyr Arg Trp Ile Val Gln Leu Pro			
130	135	140	
ggc caa acc gag ctg ccc ttt aat atc ata ctg ccc tcg ttt gcc gtg			480
Gly Gln Thr Glu Leu Pro Phe Asn Ile Ile Leu Pro Ser Phe Ala Val			
145	150	155	160
cag cca gga gtc ttt ccg ctc acc tac gtg ctg ctg acc gct tcc ggt			528
Gln Pro Gly Val Phe Pro Leu Thr Tyr Val Leu Leu Thr Ala Ser Gly			
165	170	175	
gcc tgc acc gtt ttc gcc ttc agc ttc gtg gac gga ttc ttc att tgc			576
Ala Cys Thr Val Phe Ala Phe Ser Phe Val Asp Gly Phe Phe Ile Cys			
180	185	190	
tcg tgc ctc tac atc tgc ggc gct ttc cgg ctg gtg cag cag gac att			624
Ser Cys Leu Tyr Ile Cys Gly Ala Phe Arg Leu Val Gln Gln Asp Ile			
195	200	205	
cgc agg ata ttt gcc gat ttg cat ggc gtg gat gtg ttc acc gag gag			672
Arg Arg Ile Phe Ala Asp Leu His Gly Val Asp Val Phe Thr Glu Glu			
210	215	220	
atg aac gcg gag gtg cgg cac aga ctg gcc caa gtt gtc gag cgg cac			720
Met Asn Ala Glu Val Arg His Arg Leu Ala Gln Val Val Glu Arg His			
225	230	235	240
aat gcg att atc gat ttc tgc acg gac cta aca cgc cag ttc acc gtt			768
Asn Ala Ile Ile Asp Phe Cys Thr Asp Leu Thr Arg Gln Phe Thr Val			
245	250	255	
atc gtt tta atg cat ttc ctg tcc gcc gcc ttc gtc ctc tgc tcg acc			816
Ile Val Leu Met His Phe Leu Ser Ala Ala Phe Val Leu Cys Ser Thr			
260	265	270	
atc ctg gac atc atg ttg aac acg tcg tcg ttg agc ggc tta acc tac			864
Ile Leu Asp Ile Met Leu Asn Thr Ser Ser Leu Ser Gly Leu Thr Tyr			
275	280	285	
atc tgc tat atc atc gcg gcc cta acg cag cta ttc ctc tac tgc ttc			912
Ile Cys Tyr Ile Ile Ala Ala Leu Thr Gln Leu Phe Leu Tyr Cys Phe			

290

295

300

gga ggc aat cac gtc agc gag agt agt gcg gct gtg gcg gac gtg ctg 960
 Gly Gly Asn His Val Ser Glu Ser Ser Ala Ala Val Ala Asp Val Leu
 305 310 315 320

 tac gac atg gag tgg tac aaa tgc gat gcg agg act agg aaa gtg att 1008
 Tyr Asp Met Glu Trp Tyr Lys Cys Asp Ala Arg Thr Arg Lys Val Ile
 325 330 335

 tta atg ata ttg cgc cgt tcg cag cgg gca aaa aca att gcg gtg ccg 1056
 Leu Met Ile Leu Arg Arg Ser Gln Arg Ala Lys Thr Ile Ala Val Pro
 340 345 350

 ttt ttt acg ccc tca ctg cca gca ctc cga tct ata ctc agc aca gcc 1104
 Phe Phe Thr Pro Ser Leu Pro Ala Leu Arg Ser Ile Leu Ser Thr Ala
 355 360 365

 ggc tca tat atc acg ctg cta aag acg ttc ctg taa 1140
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 370 375

<210> 4

<211> 379

<212> PRT

<213> Drosophila melanogaster

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 20 25 30

Gly Gly Gly Gly Arg Pro Trp His Ala His Leu Leu Phe Val Phe Ala
 35 40 45

Phe Ala Met Val Val Val Gly Ala Val Gly Glu Val Ser Tyr Gly Cys
 50 55 60

Val His Leu Asp Asn Leu Val Val Ala Leu Glu Ala Phe Cys Pro Gly
 65 70 75 80

Thr Thr Lys Ala Val Cys Val Leu Lys Leu Trp Val Phe Phe Arg Ser
 85 90 95

Asn Arg Arg Trp Ala Glu Leu Val Gln Arg Leu Arg Ala Ile Leu Leu

100					105					110						
Ser	Leu	Leu	Leu	Leu	Ser	Ser	Gly	Thr	Ala	Thr	Asn	Ala	Ala	Phe	Thr	
115					120					125						
Leu	Gln	Pro	Leu	Ile	Met	Gly	Leu	Tyr	Arg	Trp	Ile	Val	Gln	Leu	Pro	
130					135					140						
Gly	Gln	Thr	Glu	Leu	Pro	Phe	Asn	Ile	Ile	Leu	Pro	Ser	Phe	Ala	Val	
145					150					155					160	
Gln	Pro	Gly	Val	Phe	Pro	Leu	Thr	Tyr	Val	Leu	Leu	Thr	Ala	Ser	Gly	
165					170					175						
Ala	Cys	Thr	Val	Phe	Ala	Phe	Ser	Phe	Val	Asp	Gly	Phe	Phe	Ile	Cys	
180					185					190						
Ser	Cys	Leu	Tyr	Ile	Cys	Gly	Ala	Phe	Arg	Leu	Val	Gln	Gln	Asp	Ile	
195					200					205						
Arg	Arg	Ile	Phe	Ala	Asp	Leu	His	Gly	Val	Asp	Val	Phe	Thr	Glu	Glu	
210					215					220						
Met	Asn	Ala	Glu	Val	Arg	His	Arg	Leu	Ala	Gln	Val	Val	Glu	Arg	His	
225					230					235					240	
Asn	Ala	Ile	Ile	Asp	Phe	Cys	Thr	Asp	Leu	Thr	Arg	Gln	Phe	Thr	Val	
245					250					255						
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260					265					270						
Ile	Leu	Asp	Ile	Met	Leu	Asn	Thr	Ser	Ser	Leu	Ser	Gly	Leu	Thr	Tyr	
275					280					285						
Ile	Cys	Tyr	Ile	Ile	Ala	Ala	Leu	Thr	Gln	Leu	Phe	Leu	Tyr	Cys	Phe	
290					295					300						
Gly	Gly	Asn	His	Val	Ser	Glu	Ser	Ser	Ala	Ala	Val	Ala	Asp	Val	Leu	
305					310					315					320	
Tyr	Asp	Met	Glu	Trp	Tyr	Lys	Cys	Asp	Ala	Arg	Thr	Arg	Lys	Val	Ile	
325					330					335						
Leu	Met	Ile	Leu	Arg	Arg	Ser	Gln	Arg	Ala	Lys	Thr	Ile	Ala	Val	Pro	
340					345					350						
Phe	Phe	Thr	Pro	Ser	Leu	Pro	Ala	Leu	Arg	Ser	Ile	Leu	Ser	Thr	Ala	

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360

365

Gly Ser Tyr Ile Thr Leu Leu Lys Thr Phe Leu
370 375

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<213> *Drosophila melanogaster*

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<222> (1)..(1137)

<223> DOR23A.1, coding region of AF127925

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aat gcc tgg cga att tgt ggt gcc ttg gat ctc agc gag ggt agg tac	96
Asn Ala Trp Arg Ile Cys Gly Ala Leu Asp Leu Ser Glu Gly Arg Tyr	
20 25 30	
tgg agt tgg tcg atg cta ttg tgc atc ttg gtg tac ctg ccg aca ccc	144
Trp Ser Trp Ser Met Leu Leu Cys Ile Leu Val Tyr Leu Pro Thr Pro	
35 40 45	
atg cta ctg aga gga gta tac agt ttc gaa gat ccg gtg gaa aat aat	192
Met Leu Leu Arg Gly Val Tyr Ser Phe Glu Asp Pro Val Glu Asn Asn	
50 55 60	
ttc agc ttg agc ctg acg gtc act tcg ctg tcc aat ctc atg aag ttc	240
Phe Ser Leu Ser Leu Thr Val Thr Ser Leu Ser Asn Leu Met Lys Phe	
65 70 75 80	
tgc atg tac gtg gcc caa cta aca aag atg gtc gag gtc cag agt ctt	288
Cys Met Tyr Val Ala Gln Leu Thr Lys Met Val Glu Val Gln Ser Leu	
85 90 95	
att ggt cag ctg gat gcc cgg gtt tct ggc gag agc cag tct gag cgt	336
Ile Gly Gln Leu Asp Ala Arg Val Ser Gly Glu Ser Gln Ser Glu Arg	
100 105 110	
cat aga aat atg acc gag cac ctg cta agg atg tcc aag ctg ttc cag	384
His Arg Asn Met Thr Glu His Leu Leu Arg Met Ser Lys Leu Phe Gln	

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<212> PRT
<213> Drosophila melanogaster
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  20          25          30
Trp Ser Trp Ser Met Leu Leu Cys Ile Leu Val Tyr Leu Pro Thr Pro
  35          40          45
Met Leu Leu Arg Gly Val Tyr Ser Phe Glu Asp Pro Val Glu Asn Asn
  50          55          60
Phe Ser Leu Ser Leu Thr Val Thr Ser Leu Ser Asn Leu Met Lys Phe
  65          70          75          80
Cys Met Tyr Val Ala Gln Leu Thr Lys Met Val Glu Val Gln Ser Leu
  85          90          95
Ile Gly Gln Leu Asp Ala Arg Val Ser Gly Glu Ser Gln Ser Glu Arg
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His Arg Asn Met Thr Glu His Leu Leu Arg Met Ser Lys Leu Phe Gln
  115         120         125

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<210> 7
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 <222> (1)..(1140)
 <223> DOR 24D.1, a coding region on BDGP Clone No.
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 1 5 10 15

 ttc atg gtg cca aag ttt gca tta tcg ctg att ggt ttt tat ccc gaa 96
 Phe Met Val Pro Lys Phe Ala Leu Ser Leu Ile Gly Phe Tyr Pro Glu
 20 25 30

 cag aag cga acg gtt ttg gtg aaa ctt tgg agt ttc ttc aac ttt ttc 144
 Gln Lys Arg Thr Val Leu Val Lys Leu Trp Ser Phe Phe Asn Phe Phe
 35 40 45

 atc ctc acc tac ggc tgt tat gca gag gct tac tat ggc ata cac tat 192
 Ile Leu Thr Tyr Gly Cys Tyr Ala Glu Ala Tyr Tyr Gly Ile His Tyr
 50 55 60

 ata ccg att aac ata gcc act gca ttg gat gcc ctt tgt cct gtg gcc 240
 Ile Pro Ile Asn Ile Ala Thr Ala Leu Asp Ala Leu Cys Pro Val Ala
 65 70 75 80

 tcc agc att ttg tcg ctg gtg aaa atg gtc gcc att tgg tgg tat caa 288
 Ser Ser Ile Leu Ser Leu Val Lys Met Val Ala Ile Trp Trp Tyr Gln
 85 90 95

 gat gaa tta agg agt ttg ata gag cgg agg ttc tat aca ctg gca acg 336
 Asp Glu Leu Arg Ser Leu Ile Glu Arg Arg Phe Tyr Thr Leu Ala Thr
 100 105 110

 caa cta aca ttc ctg cta cta tgc tgt gga ttt tgc acc agt act tcc 384
 Gln Leu Thr Phe Leu Leu Leu Cys Cys Gly Phe Cys Thr Ser Thr Ser
 115 120 125

 tat tcc gtc aga cat ttg att gat aat atc ctg aga cgc acc cat ggc 432

000210 0151000

Tyr	Ser	Val	Arg	His	Leu	Ile	Asp	Asn	Ile	Leu	Arg	Arg	Thr	His	Gly		
130						135					140						
aag	gac	tgg	atc	tac	gag	act	ccg	ttc	aag	atg	atg	ttc	ccc	gat	ctt	480	
Lys	Asp	Trp	Ile	Tyr	Glu	Thr	Pro	Phe	Lys	Met	Met	Phe	Pro	Asp	Leu		
145					150					155					160		
ctc	ctg	cgt	ttg	cca	ctc	tat	ccc	atc	acc	tat	ata	ctc	gtg	cat	tgg	528	
Leu	Leu	Arg	Leu	Pro	Leu	Tyr	Pro	Ile	Thr	Tyr	Ile	Leu	Val	His	Trp		
				165					170					175			
cat	ggc	tac	att	act	gtg	ggt	tgt	ttt	gtc	ggc	gcg	gat	ggt	ttc	ttc	576	
His	Gly	Tyr	Ile	Thr	Val	Val	Cys	Phe	Val	Gly	Ala	Asp	Gly	Phe	Phe		
			180					185					190				
ctg	ggg	ttc	tgt	ttg	tac	ttc	act	gtt	ttg	ctg	ctc	tgt	ctg	cag	gac	624	
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		195					200					205					
gat	gtt	tgt	gat	tta	cta	gag	gtt	gaa	aac	atc	gag	aag	agt	ccc	tcc	672	
Asp	Val	Cys	Asp	Leu	Leu	Glu	Val	Glu	Asn	Ile	Glu	Lys	Ser	Pro	Ser		
	210					215					220						
gaa	gcg	gag	gaa	gct	cgc	ata	gtt	cgg	gaa	atg	gaa	aaa	ctg	gtg	gac	720	
Glu	Ala	Glu	Glu	Ala	Arg	Ile	Val	Arg	Glu	Met	Glu	Lys	Leu	Val	Asp		
225				230					235					240			
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Arg	His	Asn	Glu	Val	Ala	Glu	Leu	Thr	Glu	Arg	Leu	Ser	Gly	Val	Met		
			245					250					255				
gtg	gaa	ata	aca	ctg	gcc	cac	ttt	gtt	act	tcg	agt	ttg	ata	atc	gga	816	
Val	Glu	Ile	Thr	Leu	Ala	His	Phe	Val	Thr	Ser	Ser	Leu	Ile	Ile	Gly		
			260					265					270				
acc	agc	gtg	gtg	gat	att	tta	tta	ttt	tcc	ggc	ctg	gga	atc	att	gtg	864	
Thr	Ser	Val	Val	Asp	Ile	Leu	Leu	Phe	Ser	Gly	Leu	Gly	Ile	Ile	Val		
		275				280						285					
tat	gtg	gtc	tac	act	tgt	gcc	gta	ggt	gtg	gaa	ata	ttt	cta	tac	tgt	912	
Tyr	Val	Val	Tyr	Thr	Cys	Ala	Val	Gly	Val	Glu	Ile	Phe	Leu	Tyr	Cys		
	290					295					300						
tta	gga	gga	tct	cat	att	atg	gaa	gcg	tgt	tcc	aat	cta	gcg	cgc	tcc	960	
Leu	Gly	Gly	Ser	His	Ile	Met	Glu	Ala	Cys	Ser	Asn	Leu	Ala	Arg	Ser		
305					310				315					320			
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Thr Phe Ser Ser His Trp Tyr Gly His Ser Val Arg Val Gln Lys Met
 325 330 335

acc ctt ttg atg gta gct cgt gct caa cga gtt ctc aca att aaa att 1056
 Thr Leu Leu Met Val Ala Arg Ala Gln Arg Val Leu Thr Ile Lys Ile
 340 345 350

cct ttc ttt tcc cca tca tta gag act cta act tcg att ttg cgc ttc 1104
 Pro Phe Phe Ser Pro Ser Leu Glu Thr Leu Thr Ser Ile Leu Arg Phe
 355 360 365

act gga tct ctg att gcc ctg gca aag tcg gtt ata taa 1143
 Thr Gly Ser Leu Ile Ala Leu Ala Lys Ser Val Ile
 370 375 380

<210> 8

<211> 380

<212> PRT

<213> Drosophila melanogaster

<400> 8

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Phe Met Val Pro Lys Phe Ala Leu Ser Leu Ile Gly Phe Tyr Pro Glu
 20 25 30

Gln Lys Arg Thr Val Leu Val Lys Leu Trp Ser Phe Phe Asn Phe Phe
 35 40 45

Ile Leu Thr Tyr Gly Cys Tyr Ala Glu Ala Tyr Tyr Gly Ile His Tyr
 50 55 60

Ile Pro Ile Asn Ile Ala Thr Ala Leu Asp Ala Leu Cys Pro Val Ala
 65 70 75 80

Ser Ser Ile Leu Ser Leu Val Lys Met Val Ala Ile Trp Trp Tyr Gln
 85 90 95

Asp Glu Leu Arg Ser Leu Ile Glu Arg Arg Phe Tyr Thr Leu Ala Thr
 100 105 110

Gln Leu Thr Phe Leu Leu Leu Cys Cys Gly Phe Cys Thr Ser Thr Ser
 115 120 125

Tyr Ser Val Arg His Leu Ile Asp Asn Ile Leu Arg Arg Thr His Gly
 130 135 140

<210> 9
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 <213> Drosophila melanogaster

<220>
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 <222> (1)..(1209)

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ata cag tct agg gat tcg aat gca tac atg atg gag acg ctg cga aat	96
Ile Gln Ser Arg Asp Ser Asn Ala Tyr Met Met Glu Thr Leu Arg Asn	
20 25 30	
tcg ggc ttg aat ttg aag aac gat ttc ggt ata ggc cgc aag att tgg	144
Ser Gly Leu Asn Leu Lys Asn Asp Phe Gly Ile Gly Arg Lys Ile Trp	
35 40 45	
agg gtg ttt tcg ttc acc tac aat atg gtg ata ctt ccc gta agt ttc	192
Arg Val Phe Ser Phe Thr Tyr Asn Met Val Ile Leu Pro Val Ser Phe	
50 55 60	
cca atc aac tat gtg ata cat ctg gcg gag ttc ccg ccg gag ctg ctg	240
Pro Ile Asn Tyr Val Ile His Leu Ala Glu Phe Pro Pro Glu Leu Leu	
65 70 75 80	
ctg caa tcc ctg caa ctg tgc ctc aac act tgg tgc ttc gct ctg aag	288
Leu Gln Ser Leu Gln Leu Cys Leu Asn Thr Trp Cys Phe Ala Leu Lys	
85 90 95	
ttc ttc act ctg atc gtc tat acg cac cgc ttg gag ctg gcc aac aag	336
Phe Phe Thr Leu Ile Val Tyr Thr His Arg Leu Glu Leu Ala Asn Lys	
100 105 110	
cac ttt gac gaa ttg gat aag tac tgc gtg aag ccg gcg gag aag cgc	384
His Phe Asp Glu Leu Asp Lys Tyr Cys Val Lys Pro Ala Glu Lys Arg	
115 120 125	
aag gtt cgc gac atg gtg gcc act att aca aga ctg tac ctg acc ttc	432
Lys Val Arg Asp Met Val Ala Thr Ile Thr Arg Leu Tyr Leu Thr Phe	
130 135 140	
gtc gtg gtc tac gtc ctc tac gcc acc tcc acg cta ctg gac gga cta	480
Val Val Val Tyr Val Leu Tyr Ala Thr Ser Thr Leu Leu Asp Gly Leu	

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Thr Val Tyr Ala Ile Ala Ser Gly Met Asn Leu Asp Gln Lys Leu Ser
 385 390 395 400

Ile Lys Glu

<210> 11

<211> 1137

<212> DNA

<213> Drosophila melanogaster

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<222> (1)..(1134)

<223> DOR 33B.1, a coding region on BDGP Clone No.
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 1 5 10 15

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 Trp Leu Tyr Trp Arg Leu Leu Gly Val Glu Gly Asp Tyr Pro Phe Arg
 20 25 30

cgg cta gtg gat ttt aca atc acg tct ttc att acg att tta ttt ccc 144
 Arg Leu Val Asp Phe Thr Ile Thr Ser Phe Ile Thr Ile Leu Phe Pro
 35 40 45

gtg cat ctt ata ctg gga atg tat aaa aag ccc cag att caa gtc ttc 192
 Val His Leu Ile Leu Gly Met Tyr Lys Lys Pro Gln Ile Gln Val Phe
 50 55 60

agg agt ctg cat ttc aca tcg gaa tgc ctt ttc tgc agc tat aag ttt 240
 Arg Ser Leu His Phe Thr Ser Glu Cys Leu Phe Cys Ser Tyr Lys Phe
 65 70 75 80

ttc tgt ttt cgt tgg aaa ctt aaa gaa ata aag acc atc gaa gga ttg 288
 Phe Cys Phe Arg Trp Lys Leu Lys Glu Ile Lys Thr Ile Glu Gly Leu
 85 90 95

ctc cag gat ctc gat agt cga gtt gaa agt gaa gaa gaa cgc aac tac 336
 Leu Gln Asp Leu Asp Ser Arg Val Glu Ser Glu Glu Glu Arg Asn Tyr
 100 105 110

ctg atg aca atg gag ttt gat aag cta cca tat gcc atc ttc tcc agc 960
 Leu Met Thr Met Glu Phe Asp Lys Leu Pro Tyr Ala Ile Phe Ser Ser
 305 310 315 320

aac tgg ctt aaa atg gat aaa aga tac aat cga tcc ttg ata att ctg 1008
 Asn Trp Leu Lys Met Asp Lys Arg Tyr Asn Arg Ser Leu Ile Ile Leu
 325 330 335

atg caa cta aca ctg gtt cca gtg aat ata aaa gca ggt ggt att gtt 1056
 Met Gln Leu Thr Leu Val Pro Val Asn Ile Lys Ala Gly Gly Ile Val
 340 345 350

ggc atc gat atg agt gca ttt ttt gcc aca gtt cgg atg gca tat tcc 1104
 Gly Ile Asp Met Ser Ala Phe Phe Ala Thr Val Arg Met Ala Tyr Ser
 355 360 365

ttt tac act tta gcc ttg tca ttt cga gta tag 1137
 Phe Tyr Thr Leu Ala Leu Ser Phe Arg Val
 370 375

<210> 12

<211> 378

<212> PRT

<213> Drosophila melanogaster

<400> 12

Met Asp Ser Arg Arg Lys Val Arg Ser Glu Asn Leu Tyr Lys Thr Tyr
 1 5 10 15

Trp Leu Tyr Trp Arg Leu Leu Gly Val Glu Gly Asp Tyr Pro Phe Arg
 20 25 30

Arg Leu Val Asp Phe Thr Ile Thr Ser Phe Ile Thr Ile Leu Phe Pro
 35 40 45

Val His Leu Ile Leu Gly Met Tyr Lys Lys Pro Gln Ile Gln Val Phe
 50 55 60

Arg Ser Leu His Phe Thr Ser Glu Cys Leu Phe Cys Ser Tyr Lys Phe
 65 70 75 80

Phe Cys Phe Arg Trp Lys Leu Lys Glu Ile Lys Thr Ile Glu Gly Leu
 85 90 95

Leu Gln Asp Leu Asp Ser Arg Val Glu Ser Glu Glu Glu Arg Asn Tyr
 100 105 110

Phe	Asn	Gln	Asn	Pro	Ser	Arg	Val	Ala	Arg	Met	Leu	Ser	Lys	Ser	Tyr	115	120	125	
Leu	Val	Ala	Ala	Ile	Ser	Ala	Ile	Ile	Thr	Ala	Thr	Val	Ala	Gly	Leu	130	135	140	
Phe	Ser	Thr	Gly	Arg	Asn	Leu	Met	Tyr	Leu	Gly	Trp	Phe	Pro	Tyr	Asp	145	150	155	160
Phe	Gln	Ala	Thr	Ala	Ala	Ile	Tyr	Trp	Ile	Ser	Phe	Ser	Tyr	Gln	Ala	165	170	175	
Ile	Gly	Ser	Ser	Leu	Leu	Ile	Leu	Glu	Asn	Leu	Ala	Asn	Asp	Ser	Tyr	180	185	190	
Pro	Pro	Ile	Thr	Phe	Cys	Val	Val	Ser	Gly	His	Val	Arg	Leu	Leu	Ile	195	200	205	
Met	Arg	Leu	Ser	Arg	Ile	Gly	His	Asp	Val	Lys	Leu	Ser	Ser	Ser	Glu	210	215	220	
Asn	Thr	Arg	Lys	Leu	Ile	Glu	Gly	Ile	Gln	Asp	His	Arg	Lys	Leu	Met	225	230	235	240
Lys	Ile	Ile	Arg	Leu	Leu	Arg	Ser	Thr	Leu	His	Leu	Ser	Gln	Leu	Gly	245	250	255	
Gln	Phe	Leu	Ser	Ser	Gly	Ile	Asn	Ile	Ser	Ile	Thr	Leu	Ile	Asn	Ile	260	265	270	
Leu	Phe	Phe	Ala	Glu	Asn	Asn	Phe	Ala	Met	Leu	Tyr	Tyr	Ala	Val	Phe	275	280	285	
Phe	Ala	Ala	Met	Leu	Ile	Glu	Leu	Phe	Pro	Ser	Cys	Tyr	Tyr	Gly	Ile	290	295	300	
Leu	Met	Thr	Met	Glu	Phe	Asp	Lys	Leu	Pro	Tyr	Ala	Ile	Phe	Ser	Ser	305	310	315	320
Asn	Trp	Leu	Lys	Met	Asp	Lys	Arg	Tyr	Asn	Arg	Ser	Leu	Ile	Ile	Leu	325	330	335	
Met	Gln	Leu	Thr	Leu	Val	Pro	Val	Asn	Ile	Lys	Ala	Gly	Gly	Ile	Val	340	345	350	
Gly	Ile	Asp	Met	Ser	Ala	Phe	Phe	Ala	Thr	Val	Arg	Met	Ala	Tyr	Ser	355	360	365	

Phe Tyr Thr Leu Ala Leu Ser Phe Arg Val
370 375

<210> 13
<211> 1140
<212> DNA
<213> Drosophila melanogaster

<220>
<221> CDS
<222> (1)..(1137)
<223> DOR 33B.2, a coding region on BDGP Clone No.
AC006240

<400> 13
atg gac tta aaa ccg cga gtc att cga agt gaa gat atc tac aga acc 48
Met Asp Leu Lys Pro Arg Val Ile Arg Ser Glu Asp Ile Tyr Arg Thr
1 5 10 15

tat tgg tta tat tgg cat ctt ttg ggc ctg gaa agc aat ttc ttt ctg 96
Tyr Trp Leu Tyr Trp His Leu Leu Gly Leu Glu Ser Asn Phe Phe Leu
20 25 30

aat cgc ttg ttg gat ttg gtg att aca att ttc gta acc att tgg tat 144
Asn Arg Leu Leu Asp Leu Val Ile Thr Ile Phe Val Thr Ile Trp Tyr
35 40 45

cca att cac ctg att ctg gga ctg ttt atg gaa aga tct ttg ggg gat 192
Pro Ile His Leu Ile Leu Gly Leu Phe Met Glu Arg Ser Leu Gly Asp
50 55 60

gtc tgc aag ggt cta cca att acg gca gca tgc ttt ttc gcc agc ttt 240
Val Cys Lys Gly Leu Pro Ile Thr Ala Ala Cys Phe Phe Ala Ser Phe
65 70 75 80

aaa ttt att tgt ttt cgc ttc aag cta tct gaa att aaa gaa atc gaa 288
Lys Phe Ile Cys Phe Arg Phe Lys Leu Ser Glu Ile Lys Glu Ile Glu
85 90 95

ata tta ttt aaa gag ctg gat cag cga gct tta agt cga gag gaa tgc 336
Ile Leu Phe Lys Glu Leu Asp Gln Arg Ala Leu Ser Arg Glu Glu Cys
100 105 110

gag ttt ttc aat caa aat acg aga cgt gag gcg aat ttc att tgg aaa 384
Glu Phe Phe Asn Gln Asn Thr Arg Arg Glu Ala Asn Phe Ile Trp Lys
115 120 125

tca agt aac tgg atg agt atg aat cgg agc tac agc cgc atc cta ctg 1008
 Ser Ser Asn Trp Met Ser Met Asn Arg Ser Tyr Ser Arg Ile Leu Leu
 325 330 335

atc ttc atg caa ctc acc ctg gcg gaa gtg cag atc aag gcc ggt ggg 1056
 Ile Phe Met Gln Leu Thr Leu Ala Glu Val Gln Ile Lys Ala Gly Gly
 340 345 350

atg att ggc atc gga atg aac gcc ttc ttt gcc acc gtg cga ttg gcc 1104
 Met Ile Gly Ile Gly Met Asn Ala Phe Phe Ala Thr Val Arg Leu Ala
 355 360 365

tac tcc ttc ttc act ttg gcc atg tcg ctg cgt taa 1140
 Tyr Ser Phe Phe Thr Leu Ala Met Ser Leu Arg
 370 375

<210> 14
 <211> 379
 <212> PRT
 <213> Drosophila melanogaster

<400> 14
 Met Asp Leu Lys Pro Arg Val Ile Arg Ser Glu Asp Ile Tyr Arg Thr
 1 5 10 15

Tyr Trp Leu Tyr Trp His Leu Leu Gly Leu Glu Ser Asn Phe Phe Leu
 20 25 30

Asn Arg Leu Leu Asp Leu Val Ile Thr Ile Phe Val Thr Ile Trp Tyr
 35 40 45

Pro Ile His Leu Ile Leu Gly Leu Phe Met Glu Arg Ser Leu Gly Asp
 50 55 60

Val Cys Lys Gly Leu Pro Ile Thr Ala Ala Cys Phe Phe Ala Ser Phe
 65 70 75 80

Lys Phe Ile Cys Phe Arg Phe Lys Leu Ser Glu Ile Lys Glu Ile Glu
 85 90 95

Ile Leu Phe Lys Glu Leu Asp Gln Arg Ala Leu Ser Arg Glu Glu Cys
 100 105 110

Glu Phe Phe Asn Gln Asn Thr Arg Arg Glu Ala Asn Phe Ile Trp Lys
 115 120 125

Ser Phe Ile Val Ala Tyr Gly Leu Ser Asn Ile Ser Ala Ile Ala Ser
130 135 140

Val	Leu	Phe	Gly	Gly	Gly	His	Lys	Leu	Leu	Tyr	Pro	Ala	Trp	Phe	Pro
145					150					155					160

Tyr Asp Val Gln Ala Thr Glu Leu Ile Phe Trp Leu Ser Val Thr Tyr
165 170 175

Gln Ile Ala Gly Val Ser Leu Ala Ile Leu Gln Asn Leu Ala Asn Asp
180 185 - 190

Ser Tyr Pro Pro Met Thr Phe Cys Val Val Ala Gly His Val Arg Leu
195 200 205

Leu Ala Met Arg Leu Ser Arg Ile Gly Gln Gly Pro Glu Glu Thr Ile
210 215 220

Tyr Leu Thr Gly Lys Gln Leu Ile Glu Ser Ile Glu Asp His Arg Lys
225 230 235 240

Leu Met Lys Ile Val Glu Leu Leu Arg Ser Thr Met Asn Ile Ser Gln
245 250 255

Leu Gly Gln Phe Ile Ser Ser Gly Val Asn Ile Ser Ile Thr Leu Val
260 265 270

Asn Ile Leu Phe Phe Ala Asp Asn Asn Phe Ala Ile Thr Tyr Tyr Gly
275 280 285

Val Tyr Phe Leu Ser Met Val Leu Glu Leu Phe Pro Cys Cys Tyr Tyr
290 295 300

Gly Thr Leu Ile Ser Val Glu Met Asn Gln Leu Thr Tyr Ala Ile Tyr
305 310 315 320

Ser Ser Asn Trp Met Ser Met Asn Arg Ser Tyr Ser Arg Ile Leu Leu
325 330 335

Ile Phe Met Gln Leu Thr Leu Ala Glu Val Gln Ile Lys Ala Gly Gly
340 345 350

Met Ile Gly Ile Gly Met Asn Ala Phe Phe Ala Thr Val Arg Leu Ala
355 360 365

Tyr Ser Phe Phe Thr Leu Ala Met Ser Leu Arg
370 375

<210> 15
 <211> 1155
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1152)
 <223> DOR 33B3.3, a coding region on BDGP Clone No.
 AC006240

<400> 15
 atg gtc att atc gac agt ctt agt ttt tat cgt cca ttc tgg atc tgc 48
 Met Val Ile Ile Asp Ser Leu Ser Phe Tyr Arg Pro Phe Trp Ile Cys
 1 5 10 15

atg cga ttg ctg gta ccg act ttc ttc aag gat tcc tca cgt cct gtc 96
 Met Arg Leu Leu Val Pro Thr Phe Phe Lys Asp Ser Ser Arg Pro Val
 20 25 30

cag ctg tac gtg gtg ttg ctg cac atc ctg gtc acc ttg tgg ttt cca 144
 Gln Leu Tyr Val Val Leu Leu His Ile Leu Val Thr Leu Trp Phe Pro
 35 40 45

ctg cat ctg ctg ctg cat ctt ctg cta ctt cca tct acc gct gag ttc 192
 Leu His Leu Leu Leu His Leu Leu Leu Leu Pro Ser Thr Ala Glu Phe
 50 55 60

ttt aag aac ctg acc atg tct ctg act tgt gtg gcc tgc agt ctg aag 240
 Phe Lys Asn Leu Thr Met Ser Leu Thr Cys Val Ala Cys Ser Leu Lys
 65 70 75 80

cat gtg gcc cac ttg tat cac ttg ccg cag att gtg gaa atc gaa tca 288
 His Val Ala His Leu Tyr His Leu Pro Gln Ile Val Glu Ile Glu Ser
 85 90 95

ctg atc gag caa tta gac aca ttt att gcc agc gaa cag gag cat cgt 336
 Leu Ile Glu Gln Leu Asp Thr Phe Ile Ala Ser Glu Gln Glu His Arg
 100 105 110

tac tat cgg gat cac gta cat tgc cat gct agg cgc ttt aca aga tgt 384
 Tyr Tyr Arg Asp His Val His Cys His Ala Arg Arg Phe Thr Arg Cys
 115 120 125

ctc tat att agc ttt ggc atg atc tat gcg ctt ttc ctg ttc ggc gtc 432
 Leu Tyr Ile Ser Phe Gly Met Ile Tyr Ala Leu Phe Leu Phe Gly Val

130	135	140	
ttc gtt cag gtt att agc gga aat tgg gaa ctt ctc tat cca gcc tat			480
Phe Val Gln Val Ile Ser Gly Asn Trp Glu Leu Leu Tyr Pro Ala Tyr			
145	150	155	160
ttc cca ttc gac ttg gag agc aat cgc ttt ctc ggc gca gta gcc ttg			528
Phe Pro Phe Asp Leu Glu Ser Asn Arg Phe Leu Gly Ala Val Ala Leu			
	165	170	175
ggc tat cag gta ttc agc atg tta gtt gaa ggc ttc cag ggg ctg ggc			576
Gly Tyr Gln Val Phe Ser Met Leu Val Glu Gly Phe Gln Gly Leu Gly			
	180	185	190
aac gat acc tat acc cca ctg acc cta tgc ctt ctg gcc gga cat gtc			624
Asn Asp Thr Tyr Thr Pro Leu Thr Leu Cys Leu Leu Ala Gly His Val			
	195	200	205
cat ttg tgg tcc ata cga atg ggt caa ctg gga tac ttc gat gac gag			672
His Leu Trp Ser Ile Arg Met Gly Gln Leu Gly Tyr Phe Asp Asp Glu			
	210	215	220
acg gtg gtg aat cat cag cgt ttg ctg gat tac att gag cag cat aaa			720
Thr Val Val Asn His Gln Arg Leu Leu Asp Tyr Ile Glu Gln His Lys			
	225	230	235
ctc ttg gtg cga ttc cac aac ctg gtg agc cgg acc atc agc gaa gtg			768
Leu Leu Val Arg Phe His Asn Leu Val Ser Arg Thr Ile Ser Glu Val			
	245	250	255
caa ctg gtg cag ctg ggc gga tgt gga gcc act ctg tgc atc att gtc			816
Gln Leu Val Gln Leu Gly Gly Cys Gly Ala Thr Leu Cys Ile Ile Val			
	260	265	270
tcc tac atg ctc ttc ttt gtg ggc gac aca atc tcg ctg gtc tac tac			864
Ser Tyr Met Leu Phe Phe Val Gly Asp Thr Ile Ser Leu Val Tyr Tyr			
	275	280	285
ttg gtg ttc ttt gga gtg gtc tgc gtg cag ctc ttt ccc agc tgc tat			912
Leu Val Phe Phe Gly Val Val Cys Val Gln Leu Phe Pro Ser Cys Tyr			
	290	295	300
ttt gcc agc gaa gta gcc gag gag ttg gaa cgg ctg cca tat gcg atc			960
Phe Ala Ser Glu Val Ala Glu Glu Leu Glu Arg Leu Pro Tyr Ala Ile			
	305	310	315
ttc tcc agc aga tgg tac gat caa tcg cgg gat cat cga ttc gat ttg			1008
Phe Ser Ser Arg Trp Tyr Asp Gln Ser Arg Asp His Arg Phe Asp Leu			

335

taq	1155
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<213> Drosophila melanogaster

Leu Tyr Ile Ser Phe Gly Met Ile Tyr Ala Leu Phe Leu Phe Gly Val

130		135		140
Phe Val Gln Val Ile Ser Gly Asn Trp Glu Leu Leu Tyr Pro Ala Tyr				
145		150		155 160
Phe Pro Phe Asp Leu Glu Ser Asn Arg Phe Leu Gly Ala Val Ala Leu				
	165		170	175
Gly Tyr Gln Val Phe Ser Met Leu Val Glu Gly Phe Gln Gly Leu Gly				
	180		185	190
Asn Asp Thr Tyr Thr Pro Leu Thr Leu Cys Leu Leu Ala Gly His Val				
	195		200	205
His Leu Trp Ser Ile Arg Met Gly Gln Leu Gly Tyr Phe Asp Asp Glu				
	210		215	220
Thr Val Val Asn His Gln Arg Leu Leu Asp Tyr Ile Glu Gln His Lys				
	225		230	235 240
Leu Leu Val Arg Phe His Asn Leu Val Ser Arg Thr Ile Ser Glu Val				
	245		250	255
Gln Leu Val Gln Leu Gly Gly Cys Gly Ala Thr Leu Cys Ile Ile Val				
	260		265	270
Ser Tyr Met Leu Phe Phe Val Gly Asp Thr Ile Ser Leu Val Tyr Tyr				
	275		280	285
Leu Val Phe Phe Gly Val Val Cys Val Gln Leu Phe Pro Ser Cys Tyr				
	290		295	300
Phe Ala Ser Glu Val Ala Glu Glu Leu Glu Arg Leu Pro Tyr Ala Ile				
	305		310	315 320
Phe Ser Ser Arg Trp Tyr Asp Gln Ser Arg Asp His Arg Phe Asp Leu				
	325		330	335
Leu Ile Phe Thr Gln Leu Thr Leu Gly Asn Arg Gly Trp Ile Ile Lys				
	340		345	350
Ala Gly Gly Leu Ile Glu Leu Asn Leu Asn Ala Phe Phe Ala Thr Leu				
	355		360	365
Lys Met Ala Tyr Ser Leu Phe Ala Val Val Val Arg Ala Lys Gly Ile				
	370		375	380

<210> 17
 <211> 1152
 <212> DNA
 <213> Drosophila melanogaster

 <220>
 <221> CDS
 <222> (1)..(1149)
 <223> DOR 43B.1, coding region of AF127926

<400> 17
 atg aca atc gag gat atc ggc ctg gtg ggc atc aac gtg cgg atg tgg 48
 Met Thr Ile Glu Asp Ile Gly Leu Val Gly Ile Asn Val Arg Met Trp
 1 5 10 15

 cga cac ttg gcc gtg ctg tac ccc act ccg ggc tcc agc tgg cgc aag 96
 Arg His Leu Ala Val Leu Tyr Pro Thr Pro Gly Ser Ser Trp Arg Lys
 20 25 30

 ttc gcc ttc gtg ctg ccg gtg act gcg atg aat ctg atg cag ttc gtc 144
 Phe Ala Phe Val Leu Pro Val Thr Ala Met Asn Leu Met Gln Phe Val
 35 40 45

 tac ctg ctg cgg atg tgg ggc gac ctg ccc gcc ttc att ctg aac atg 192
 Tyr Leu Leu Arg Arg Met Trp Gly Asp Leu Pro Ala Phe Ile Leu Asn Met
 50 55 60

 ttc ttc ttc tcg gcc att ttc aac gcc ctg atg cgc acg tgg ctg gtc 240
 Phe Phe Phe Ser Ala Ile Phe Asn Ala Leu Met Arg Thr Trp Leu Val
 65 70 75 80

 ata atc aag cgg cgc cag ttc gag gag ttt ctc ggc caa ctg gcc act 288
 Ile Ile Lys Arg Arg Gln Phe Glu Glu Phe Leu Gly Gln Leu Ala Thr
 85 90 95

 ctg ttc cat tcg att ctc gac tcc acc gac gag tgg ggg cgt gcc atc 336
 Leu Phe His Ser Ile Leu Asp Ser Thr Asp Glu Trp Gly Arg Gly Ile
 100 105 110

 ctg cgg agg gcg gaa cgg gag gct cgg aac ctg gcc atc ctt aat ttg 384
 Leu Arg Arg Ala Glu Arg Glu Ala Arg Asn Leu Ala Ile Leu Asn Leu
 115 120 125

 agt gcc tcc ttc ctg gac att gtc ggt gct ctg ttt ttc gaa tat aaa 432
 Ser Ala Ser Phe Leu Asp Ile Val Gly Ala Leu Phe Phe Glu Tyr Lys
 130 135 140

ctc ctg atc ttc ttg atg caa aca caa cac ccg atg gag ata aga gtc 1056
 Leu Leu Ile Phe Leu Met Gln Thr Gln His Pro Met Glu Ile Arg Val
 340 345 350

ggc aac gtt tac ccc atg aca ttg gcc atg ttc cag agt ctg ttg aat 1104
 Gly Asn Val Tyr Pro Met Thr Leu Ala Met Phe Gln Ser Leu Leu Asn
 355 360 365

gcg tcc tac tcc tac ttt acc atg ctg cgt ggc gtc acc ggc aaa tga 1152
 Ala Ser Tyr Ser Tyr Phe Thr Met Leu Arg Gly Val Thr Gly Lys
 370 375 380

<210> 18

<211> 383

<212> PRT

<213> Drosophila melanogaster

<400> 18

Met Thr Ile Glu Asp Ile Gly Leu Val Gly Ile Asn Val Arg Met Trp
 1 5 10 15

Arg His Leu Ala Val Leu Tyr Pro Thr Pro Gly Ser Ser Trp Arg Lys
 20 25 30

Phe Ala Phe Val Leu Pro Val Thr Ala Met Asn Leu Met Gln Phe Val
 35 40 45

Tyr Leu Leu Arg Met Trp Gly Asp Leu Pro Ala Phe Ile Leu Asn Met
 50 55 60

Phe Phe Phe Ser Ala Ile Phe Asn Ala Leu Met Arg Thr Trp Leu Val
 65 70 75 80

Ile Ile Lys Arg Arg Gln Phe Glu Glu Phe Leu Gly Gln Leu Ala Thr
 85 90 95

Leu Phe His Ser Ile Leu Asp Ser Thr Asp Glu Trp Gly Arg Gly Ile
 100 105 110

Leu Arg Arg Ala Glu Arg Glu Ala Arg Asn Leu Ala Ile Leu Asn Leu
 115 120 125

Ser Ala Ser Phe Leu Asp Ile Val Gly Ala Leu Phe Phe Glu Tyr Lys
 130 135 140

Phe Pro Ile Gly Val Val Thr Phe Phe Leu Pro Ala His Pro Phe Gly
 145 150 155 160

Leu Ala Leu Pro Gly Val Ser Met Thr Ser Ser Pro Val Tyr Glu Val
 165 170 175

Ile Tyr Leu Ala Gln Leu Pro Thr Pro Leu Leu Leu Ser Met Met Tyr
 180 185 190

Met Pro Phe Val Ser Leu Phe Ala Gly Leu Ala Ile Phe Gly Lys Ala
 195 200 205

Met Leu Gln Ile Leu Val His Arg Leu Gly Gln Ile Gly Gly Glu Glu
 210 215 220

Gln Ser Glu Glu Glu Arg Phe Gln Arg Leu Ala Ser Cys Ile Ala Tyr
 225 230 235 240

His Thr Gln Val Met Arg Tyr Val Trp Gln Leu Asn Lys Leu Val Ala
 245 250 255

Asn Ile Val Ala Val Glu Ala Ile Ile Phe Gly Ser Ile Ile Cys Ser
 260 265 270

Leu Leu Phe Cys Leu Asn Ile Ile Thr Ser Pro Thr Gln Val Ile Ser
 275 280 285

Ile Val Met Tyr Ile Leu Thr Met Leu Tyr Val Leu Phe Thr Tyr Tyr
 290 295 300

Asn Arg Ala Asn Glu Ile Cys Leu Glu Asn Asn Arg Val Ala Glu Ala
 305 310 315 320

Val Tyr Asn Val Pro Trp Tyr Glu Ala Gly Thr Arg Phe Arg Lys Thr
 325 330 335

Leu Leu Ile Phe Leu Met Gln Thr Gln His Pro Met Glu Ile Arg Val
 340 345 350

Gly Asn Val Tyr Pro Met Thr Leu Ala Met Phe Gln Ser Leu Leu Asn
 355 360 365

Ala Ser Tyr Ser Tyr Phe Thr Met Leu Arg Gly Val Thr Gly Lys
 370 375 380

<210> 19

<211> 1158

<212> DNA

003210 2256700

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1155)

<223> DOR 46F.1, a coding region on BDGP Clone No.
AC005974

<400> 19

atg agc aaa gga gta gaa atc ttt tac aag ggc cag aag gca ttc ttg	48
Met Ser Lys Gly Val Glu Ile Phe Tyr Lys Gly Gln Lys Ala Phe Leu	
1 5 10 15	

aac atc ctc tcg ttg tgg cct cag ata gaa cgc cgg tgg aga atc atc	96
Asn Ile Leu Ser Leu Trp Pro Gln Ile Glu Arg Arg Trp Arg Ile Ile	
20 25 30	

cac cag gtg aac tat gtc cac gta att gtg ttt tgg gtg ctg ctc ttt	144
His Gln Val Asn Tyr Val His Val Ile Val Phe Trp Val Leu Leu Phe	
35 40 45	

gat ctc ctc ttg gtg ctc cat gtg atg gct aat ttg agc tac atg tcc	192
Asp Leu Leu Leu Val Leu His Val Met Ala Asn Leu Ser Tyr Met Ser	
50 55 60	

gag gtt gtg aaa gcc atc ttt atc ctg gcc acc agt gca ggg cac acc	240
Glu Val Val Lys Ala Ile Phe Ile Leu Ala Thr Ser Ala Gly His Thr	
65 70 75 80	

acc aag ctg ctg tcc ata aag gcg aac aat gtg cag atg gag gag ctc	288
Thr Lys Leu Leu Ser Ile Lys Ala Asn Asn Val Gln Met Glu Glu Leu	
85 90 95	

ttt agg aga ttg gat aac gaa gag ttc cgt cct aga ggc gcc aac gaa	336
Phe Arg Arg Leu Asp Asn Glu Glu Phe Arg Pro Arg Gly Ala Asn Glu	
100 105 110	

gag ttg atc ttt gca gca gcc tgt gaa aga agt agg aag ctt cgg gac	384
Glu Leu Ile Phe Ala Ala Ala Cys Glu Arg Ser Arg Lys Leu Arg Asp	
115 120 125	

ttc tat gga gcg ctt tcg ttt gcc gcc ttg agc atg att ctc ata ccc	432
Phe Tyr Gly Ala Leu Ser Phe Ala Ala Leu Ser Met Ile Leu Ile Pro	
130 135 140	

cag ttc gcc ttg gac tgg tcc cac ctt ccg ctc aaa aca tac aat ccg	480
Gln Phe Ala Leu Asp Trp Ser His Leu Pro Leu Lys Thr Tyr Asn Pro	
145 150 155 160	

cca agt ctt ggt ttt gac tta atg ctc ttc agc tcg .gtg agt tct ttc 1104
 Pro Ser Leu Gly Phe Asp Leu Met Leu Phe Ser Ser Val Ser Ser Phe
 355 360 365

cgt gtt ttg act ttt ttg tgc act gta gcc aat ttc cat aat gag gct 1152
 Arg Val Leu Thr Phe Leu Cys Thr Val Ala Asn Phe His Asn Glu Ala
 370 375 380

cat tag 1158
 His
 385

<210> 20

<211> 385

<212> PRT

<213> Drosophila melanogaster

<400> 20

Met Ser Lys Gly Val Glu Ile Phe Tyr Lys Gly Gln Lys Ala Phe Leu
 1 5 10 15

Asn Ile Leu Ser Leu Trp Pro Gln Ile Glu Arg Arg Trp Arg Ile Ile
 20 25 30

His Gln Val Asn Tyr Val His Val Ile Val Phe Trp Val Leu Leu Phe
 35 40 45

Asp Leu Leu Leu Val Leu His Val Met Ala Asn Leu Ser Tyr Met Ser
 50 55 60

Glu Val Val Lys Ala Ile Phe Ile Leu Ala Thr Ser Ala Gly His Thr
 65 70 75 80

Thr Lys Leu Leu Ser Ile Lys Ala Asn Asn Val Gln Met Glu Glu Leu
 85 90 95

Phe Arg Arg Leu Asp Asn Glu Glu Phe Arg Pro Arg Gly Ala Asn Glu
 100 105 110

Glu Leu Ile Phe Ala Ala Ala Cys Glu Arg Ser Arg Lys Leu Arg Asp
 115 120 125

Phe Tyr Gly Ala Leu Ser Phe Ala Ala Leu Ser Met Ile Leu Ile Pro
 130 135 140

Gln Phe Ala Leu Asp Trp Ser His Leu Pro Leu Lys Thr Tyr Asn Pro

<210> 21
 <211> 1155
 <212> DNA
 <213> Drosophila melanogaster

 <220>
 <221> CDS
 <222> (1)..(1152)
 <223> DOR 46F.2, a coding region on BDGP Clone No.
 AC005974

<400> 21
 atg gtt acg gag gac ttt tat aag tac cag gtg tgg tac ttc caa atc 48
 Met Val Thr Glu Asp Phe Tyr Lys Tyr Gln Val Trp Tyr Phe Gln Ile
 1 5 10 15

 ctt ggt gtt tgg cag ctc ccc act tgg gcc gca gac cac cag cgt cgt 96
 Leu Gly Val Trp Gln Leu Pro Thr Trp Ala Ala Asp His Gln Arg Arg
 20 25 30

 ttt cag tcc atg agg ttt ggc ttc atc ctg gtc atc ctg ttc atc atg 144
 Phe Gln Ser Met Arg Phe Gly Phe Ile Leu Val Ile Leu Phe Ile Met
 35 40 45

 ctg ctg ctt ttc tcc ttc gaa atg ttg aac aac att tcc caa gtt agg 192
 Leu Leu Leu Phe Ser Phe Glu Met Leu Asn Asn Ile Ser Gln Val Arg
 50 55 60

 gag atc cta aag gta ttc ttc atg ttc gcc acg gaa ata tcc tgc atg 240
 Glu Ile Leu Lys Val Phe Phe Met Phe Ala Thr Glu Ile Ser Cys Met
 65 70 75 80

 gcc aaa tta ttg cat ttg aag ttg aag agc cgc aaa ctc gct ggc ttg 288
 Ala Lys Leu Leu His Leu Lys Leu Lys Ser Arg Lys Leu Ala Gly Leu
 85 90 95

 gtt gat gcg atg ttg tcc cca gag ttc ggc gtt aaa agt gaa cag gaa 336
 Val Asp Ala Met Leu Ser Pro Glu Phe Gly Val Lys Ser Glu Gln Glu
 100 105 110

 atg cag atg ctg gaa ttg gat aga gtg gcg gtt gtc cgc atg agg aac 384
 Met Gln Met Leu Glu Leu Asp Arg Val Ala Val Val Arg Met Arg Asn
 115 120 125

 tcc tac ggc atc atg tcc ctg ggc gcg gct tcc ctg atc ctt ata gtt 432
 Ser Tyr Gly Ile Met Ser Leu Gly Ala Ala Ser Leu Ile Leu Ile Val
 130 135 140

ccc tgt ttc gac aac ttt ggc gag cta cca ctg gcc atg ttg gag gta	480
Pro Cys Phe Asp Asn Phe Gly Glu Leu Pro Leu Ala Met Leu Glu Val	
145 150 155 160	
tgc agc atc gag gga tgg atc tgc tat tgg tcg cag tac ctt ttc cac	528
Cys Ser Ile Glu Gly Trp Ile Cys Tyr Trp Ser Gln Tyr Leu Phe His	
165 170 175	
tcg att tgc ctg ctg ccc act tgt gtg ctg aat ata acc tac gac tcg	576
Ser Ile Cys Leu Leu Pro Thr Cys Val Leu Asn Ile Thr Tyr Asp Ser	
180 185 190	
gtg gcc tac tcg ttg ctc tgt ttc ttg aag gtt cag cta caa atg ctg	624
Val Ala Tyr Ser Leu Leu Cys Phe Leu Lys Val Gln Leu Gln Met Leu	
195 200 205	
gtc ctg cga tta gaa aag ttg ggt cct gtg atc gaa ccc cag gat aat	672
Val Leu Arg Leu Glu Lys Leu Gly Pro Val Ile Glu Pro Gln Asp Asn	
210 215 220	
gag aaa atc gca atg gaa ctg cgt gag tgt gcc gcc tac tac aac agg	720
Glu Lys Ile Ala Met Glu Leu Arg Glu Cys Ala Ala Tyr Tyr Asn Arg	
225 230 235 240	
att gtt cgt ttc aag gac ctg gtg gag ctg ttc ata aag ggg cca gga	768
Ile Val Arg Phe Lys Asp Leu Val Glu Leu Phe Ile Lys Gly Pro Gly	
245 250 255	
tct gtg cag ctc atg tgt tct gtt ctg gtg ctg gtg tcc aac ctg tac	816
Ser Val Gln Leu Met Cys Ser Val Leu Val Leu Val Ser Asn Leu Tyr	
260 265 270	
gac atg tcc acc atg tcc att gca aac ggc gat gcc atc ttt atg ctc	864
Asp Met Ser Thr Met Ser Ile Ala Asn Gly Asp Ala Ile Phe Met Leu	
275 280 285	
aag acc tgt atc tat cag ctg gtg atg ctc tgg cag atc ttc atc att	912
Lys Thr Cys Ile Tyr Gln Leu Val Met Leu Trp Gln Ile Phe Ile Ile	
290 295 300	
tgc tac gcc tcc aac gag gta act gtc cag agc tct agg ttg tgt cac	960
Cys Tyr Ala Ser Asn Glu Val Thr Val Gln Ser Ser Arg Leu Cys His	
305 310 315 320	
agc atc tac agc tcc caa tgg acg gga tgg aac agg gca aac cgc cgg	1008
Ser Ile Tyr Ser Ser Gln Trp Thr Gly Trp Asn Arg Ala Asn Arg Arg	
325 330 335	

Pro Cys Phe Asp Asn Phe Gly Glu Leu Pro Leu Ala Met Leu Glu Val
145 150 155 160

Cys Ser Ile Glu Gly Trp Ile Cys Tyr Trp Ser Gln Tyr Leu Phe His
165 170 175

Ser Ile Cys Leu Leu Pro Thr Cys Val Leu Asn Ile Thr Tyr Asp Ser
180 185 190

Val Ala Tyr Ser Leu Leu Cys Phe Leu Lys Val Gln Leu Gln Met Leu
195 200 205

Val Leu Arg Leu Glu Lys Leu Gly Pro Val Ile Glu Pro Gln Asp Asn
210 215 220

Glu Lys Ile Ala Met Glu Leu Arg Glu Cys Ala Ala Tyr Tyr Asn Arg
225 230 235 240

Ile Val Arg Phe Lys Asp Leu Val Glu Leu Phe Ile Lys Gly Pro Gly
245 250 255

Ser Val Gln Leu Met Cys Ser Val Leu Val Leu Val Ser Asn Leu Tyr
260 265 270

Asp Met Ser Thr Met Ser Ile Ala Asn Gly Asp Ala Ile Phe Met Leu
275 280 285

Lys Thr Cys Ile Tyr Gln Leu Val Met Leu Trp Gln Ile Phe Ile Ile
290 295 300

Cys Tyr Ala Ser Asn Glu Val Thr Val Gln Ser Ser Arg Leu Cys His
305 310 315 320

Ser Ile Tyr Ser Ser Gln Trp Thr Gly Trp Asn Arg Ala Asn Arg Arg
325 330 335

Ile Val Leu Leu Met Met Gln Arg Phe Asn Ser Pro Met Leu Leu Ser
340 345 350

Thr Phe Asn Pro Thr Phe Ala Phe Ser Leu Glu Ala Phe Gly Ser Ile
355 360 365

Val Asn Cys Ser Tyr Ser Tyr Phe Ala Leu Leu Lys Arg Val Asn Ser
370 375 380

<210> 23
 <211> 1158
 <212> DNA
 <213> Drosophila melanogaster

 <220>
 <221> CDS
 <222> (1)..(1155)
 <223> DOR 47E.1, coding region of AF156880

<400> 23
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 Met Asp Ser Phe Leu Gln Val Gln Lys Ser Thr Ile Ala Leu Leu Gly
 1 5 10 15

 ttt gat ctc ttt agt gaa aat cga gaa atg tgg aaa cgc ccc tat aga 96
 Phe Asp Leu Phe Ser Glu Asn Arg Glu Met Trp Lys Arg Pro Tyr Arg
 20 25 30

 gca atg aat gtg ttt agc ata gct gcc att ttt ccc ttt atc ctg gca 144
 Ala Met Asn Val Phe Ser Ile Ala Ala Ile Phe Pro Phe Ile Leu Ala
 35 40 45

 gct gtg ctc cat aat tgg aag aat gta ttg ctg ctg gcc gat gcc atg 192
 Ala Val Leu His Asn Trp Lys Asn Val Leu Leu Leu Ala Asp Ala Met
 50 55 60

 gtg gcc cta cta ata acc att ctg ggc cta ttc aag ttt agc atg ata 240
 Val Ala Leu Leu Ile Thr Ile Leu Gly Leu Phe Lys Phe Ser Met Ile
 65 70 75 80

 ctt tac tta cgt cgc gat ttc aag cga ctg att gac aaa ttt cgt ttg 288
 Leu Tyr Leu Arg Arg Asp Phe Lys Arg Leu Ile Asp Lys Phe Arg Leu
 85 90 95

 ctc atg tcg aat gag gcg gaa cag ggc gag gaa tac gcc gag att ctc 336
 Leu Met Ser Asn Glu Ala Glu Gln Gly Glu Glu Tyr Ala Glu Ile Leu
 100 105 110

 aac gca gca aac aag cag gat caa cga atg tgc act ctg ttt agg act 384
 Asn Ala Ala Asn Lys Gln Asp Gln Arg Met Cys Thr Leu Phe Arg Thr
 115 120 125

 tgt ttc ctc ctc gcc tgg gcc ttg aat agt gtt ctg ccc ctc gtg aga 432
 Cys Phe Leu Leu Ala Trp Ala Leu Asn Ser Val Leu Pro Leu Val Arg
 130 135 140

 atg ggt ctc agc tat tgg tta gca ggt cat gca gag ccc gag ttg cct 480

Ser Ile Cys Arg Ser Leu Leu Ile Ser Met Met Arg Ala His Arg Gly
 340 345 350

ttc cgc att acg gga tac ttt ttc gag gca aac atg gag gcc ttc tca 1104
 Phe Arg Ile Thr Gly Tyr Phe Phe Glu Ala Asn Met Glu Ala Phe Ser
 355 360 365

tcg att gtt cgc acg gcg atg tcc tac atc aca atg ctg aga tca ttc 1152
 Ser Ile Val Arg Thr Ala Met Ser Tyr Ile Thr Met Leu Arg Ser Phe
 370 375 380

tcc taa 1158
 Ser
 385

<210> 24
 <211> 385
 <212> PRT
 <213> Drosophila melanogaster

<400> 24
 Met Asp Ser Phe Leu Gln Val Gln Lys Ser Thr Ile Ala Leu Leu Gly
 1 5 10 15

Phe Asp Leu Phe Ser Glu Asn Arg Glu Met Trp Lys Arg Pro Tyr Arg
 20 25 30

Ala Met Asn Val Phe Ser Ile Ala Ala Ile Phe Pro Phe Ile Leu Ala
 35 40 45

Ala Val Leu His Asn Trp Lys Asn Val Leu Leu Leu Ala Asp Ala Met
 50 55 60

Val Ala Leu Leu Ile Thr Ile Leu Gly Leu Phe Lys Phe Ser Met Ile
 65 70 75 80

Leu Tyr Leu Arg Arg Asp Phe Lys Arg Leu Ile Asp Lys Phe Arg Leu
 85 90 95

Leu Met Ser Asn Glu Ala Glu Gln Gly Glu Glu Tyr Ala Glu Ile Leu
 100 105 110

Asn Ala Ala Asn Lys Gln Asp Gln Arg Met Cys Thr Leu Phe Arg Thr
 115 120 125

Cys Phe Leu Leu Ala Trp Ala Leu Asn Ser Val Leu Pro Leu Val Arg
 130 135 140

Met Gly Leu Ser Tyr Trp Leu Ala Gly His Ala Glu Pro Glu Leu Pro
145 150 155 160

Phe Pro Cys Leu Phe Pro Trp Asn Ile His Ile Ile Arg Asn Tyr Val
165 170 175

Leu Ser Phe Ile Trp Ser Ala Phe Ala Ser Thr Gly Val Val Leu Pro
180 185 190

Ala Val Ser Leu Asp Thr Ile Phe Cys Ser Phe Thr Ser Asn Leu Cys
195 200 205

Ala Phe Phe Lys Ile Ala Gln Tyr Lys Val Val Arg Phe Lys Gly Gly
210 215 220

Ser Leu Lys Glu Ser Gln Ala Thr Leu Asn Lys Val Phe Ala Leu Tyr
225 230 235 240

Gln Thr Ser Leu Asp Met Cys Asn Asp Leu Asn Gln Cys Tyr Gln Pro
245 250 255

Ile Ile Cys Ala Gln Phe Phe Ile Ser Ser Leu Gln Leu Cys Met Leu
260 265 270

Gly Tyr Leu Phe Ser Ile Thr Phe Ala Gln Thr Glu Gly Val Tyr Tyr
275 280 285

Ala Ser Phe Ile Ala Thr Ile Ile Ile Gln Ala Tyr Ile Tyr Cys Tyr
290 295 300

Cys Gly Glu Asn Leu Lys Thr Glu Ser Ala Ser Phe Glu Trp Ala Ile
305 310 315 320

Tyr Asp Ser Pro Trp His Glu Ser Leu Gly Ala Gly Gly Ala Ser Thr
325 330 335

Ser Ile Cys Arg Ser Leu Leu Ile Ser Met Met Arg Ala His Arg Gly
340 345 350

Phe Arg Ile Thr Gly Tyr Phe Phe Glu Ala Asn Met Glu Ala Phe Ser
355 360 365

Ser Ile Val Arg Thr Ala Met Ser Tyr Ile Thr Met Leu Arg Ser Phe
370 375 380

Ser
385

<210> 25
 <211> 1203
 <212> DNA
 <213> Drosophila melanogaster

 <220>
 <221> CDS
 <222> (1)..(1200)
 <223> DOR 47E.2, a coding region on BDGP Clone No.
 AC005638

<400> 25
 atg aac gac tcg ggt tat caa tca aat ctc agc ctt ctg cgg gtt ttt 48
 Met Asn Asp Ser Gly Tyr Gln Ser Asn Leu Ser Leu Leu Arg Val Phe
 1 5 10 15

 ctc gac gag ttc cga tcg gtt ctg cgg cag gaa agt ccc ggt ctc atc 96
 Leu Asp Glu Phe Arg Ser Val Leu Arg Gln Glu Ser Pro Gly Leu Ile
 20 25 30

 cca cgc ctg gct ttt tac tat gtt cgc gcc ttt ctg agc ttg ccc ctg 144
 Pro Arg Leu Ala Phe Tyr Tyr Val Arg Ala Phe Leu Ser Leu Pro Leu
 35 40 45

 tac cga tgg atc aac ttg ttc atc atg tgc aat gtg atg acc att ttc 192
 Tyr Arg Trp Ile Asn Leu Phe Ile Met Cys Asn Val Met Thr Ile Phe
 50 55 60

 tgg acc atg ttc gtg gcc ctg ccc gag tcg aag aac gtg atc gaa atg 240
 Trp Thr Met Phe Val Ala Leu Pro Glu Ser Lys Asn Val Ile Glu Met
 65 70 75 80

 ggc gac gac ttg gtt tgg att tcg ggg atg gca ctg gtg ttc acc aag 288
 Gly Asp Asp Leu Val Trp Ile Ser Gly Met Ala Leu Val Phe Thr Lys
 85 90 95

 atc ttt tac atg cat ttg cgt tgc gac gag atc gat gaa ctt att tcg 336
 Ile Phe Tyr Met His Leu Arg Cys Asp Glu Ile Asp Glu Leu Ile Ser
 100 105 110

 gat ttt gaa tac tac aac cgg gag ctg aga ccc cat aat atc gat gag 384
 Asp Phe Glu Tyr Tyr Asn Arg Glu Leu Arg Pro His Asn Ile Asp Glu
 115 120 125

 gag gtg ttg ggt tgg cag aga ctg tgc tac gtg ata gaa tcg ggt cta 432

Glu Val Leu Gly Trp Gln Arg Leu Cys Tyr Val Ile Glu Ser Gly Leu	
130 135 140	
tat atc aac tgc ttt tgc ctg gtc aac ttc ttc agt gcc gct att ttc	480
Tyr Ile Asn Cys Phe Cys Leu Val Asn Phe Phe Ser Ala Ala Ile Phe	
145 150 155 160	
ctg caa cct ctg ttg ggc gag gga aag ctg ccc ttc cac agc gtc tat	528
Leu Gln Pro Leu Leu Gly Glu Gly Lys Leu Pro Phe His Ser Val Tyr	
165 170 175	
ccg ttt caa tgg cat cgc ttg gat ctg cat ccc tac acg ttc tgg ttc	576
Pro Phe Gln Trp His Arg Leu Asp Leu His Pro Tyr Thr Phe Trp Phe	
180 185 190	
ctc tac atc tgg cag agt ctg acc tcg cag cac aac cta atg agc att	624
Leu Tyr Ile Trp Gln Ser Leu Thr Ser Gln His Asn Leu Met Ser Ile	
195 200 205	
cta atg gtg gat atg gta ggc att tcc acg ttc ctc cag acg gcg ctc	672
Leu Met Val Asp Met Val Gly Ile Ser Thr Phe Leu Gln Thr Ala Leu	
210 215 220	
aat ctc aag ttg ctt tgc atc gag ata agg aaa ctg ggg gac atg gag	720
Asn Leu Lys Leu Leu Cys Ile Glu Ile Arg Lys Leu Gly Asp Met Glu	
225 230 235 240	
gtc agt gat aag agg ttc cac gag gag ttt tgt cgt gtg gtt cgc ttc	768
Val Ser Asp Lys Arg Phe His Glu Glu Phe Cys Arg Val Val Arg Phe	
245 250 255	
cac cag cac att atc aaa ttg gtg ggg aaa gcc aat aga gct ttc aat	816
His Gln His Ile Ile Lys Leu Val Gly Lys Ala Asn Arg Ala Phe Asn	
260 265 270	
ggc gcc ttc aat gca caa tta atg gcc agt ttc tcc ctg att tcc ata	864
Gly Ala Phe Asn Ala Gln Leu Met Ala Ser Phe Ser Leu Ile Ser Ile	
275 280 285	
tcc act ttc gag acc atg gct gca gcg gct gtg gat ccc aaa atg gcc	912
Ser Thr Phe Glu Thr Met Ala Ala Ala Val Asp Pro Lys Met Ala	
290 295 300	
gcc aag ttc gtg ctt ctc atg ctg gtg gca ttc att caa ctg tcg ctt	960
Ala Lys Phe Val Leu Leu Met Leu Val Ala Phe Ile Gln Leu Ser Leu	
305 310 315 320	
tgg tgc gtc tct gga act ttg gtt tat act cag tca gtg gag gtg gct	1008

Tyr Val Ala Glu Pro Phe Leu Pro Phe Thr Leu Gly Thr Tyr Met Leu
370 375 380

Val Leu Lys Asn Cys Tyr Arg Leu Leu Ala Leu Met Gln Glu Ser Met
385 390 395 400

<210> 27
<211> 1140
<212> DNA
<213> Drosophila melanogaster

<220>
<221> CDS
<222> (1)..(1137)
<223> DOR 59D.1, a coding region on BDGP Clone No.
AC005672

<400> 27
atg gca gag gtc aga gtg gac agt ctg gag ttt ttc aag agc cat tgg 48
Met Ala Glu Val Arg Val Asp Ser Leu Glu Phe Phe Lys Ser His Trp
1 5 10 15

acc gcc tgg cgg tac ttg gga gtg gct cat ttt cgg gtc gag aac tgg 96
Thr Ala Trp Arg Tyr Leu Gly Val Ala His Phe Arg Val Glu Asn Trp
20 25 30

aag aac ctt tac gtg ttt tac agc att gtg tcg aat ctt ctc gtg acc 144
Lys Asn Leu Tyr Val Phe Tyr Ser Ile Val Ser Asn Leu Leu Val Thr
35 40 45

ctg tgc tac ccc gtt cac ctg gga ata tcc ctc ttt cgc aac cgc acc 192
Leu Cys Tyr Pro Val His Leu Gly Ile Ser Leu Phe Arg Asn Arg Thr
50 55 60

atc acc gag gac atc ctc aac ctg acc acc ttt gcg acc tgc aca gcc 240
Ile Thr Glu Asp Ile Leu Asn Leu Thr Thr Phe Ala Thr Cys Thr Ala
65 70 75 80

tgt tcg gtg aag tgc ctg ctc tac gcc tac aac atc aag gat gtg ctg 288
Cys Ser Val Lys Cys Leu Leu Tyr Ala Tyr Asn Ile Lys Asp Val Leu
85 90 95

gag atg gag cgg ctg ttg agg ctt ttg gat gaa cgc gtc gtg ggt ccg 336
Glu Met Glu Arg Leu Leu Arg Leu Leu Asp Glu Arg Val Val Gly Pro
100 105 110

Ser Leu Phe Thr Ile Ile Ile Arg Met Arg Lys
370 375

<210> 29

<211> 1194

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1194)

<223> DOR 2F.1, coding region of NCBI Accession No.
AL009195

<400> 29

atg gag aag caa gag gat ttc aaa ctg aac acc cac agt gct gtg tac 48
Met Glu Lys Gln Glu Asp Phe Lys Leu Asn Thr His Ser Ala Val Tyr
1 5 10 15

tac cac tgg cgc gtt tgg gag ctc act ggc ctg atg cgt cct ccg ggc 96
Tyr His Trp Arg Val Trp Glu Leu Thr Gly Leu Met Arg Pro Pro Gly
20 25 30

gtt tca agc ctg ctt tac gtg gta tac tcc att acg gtc aac ttg gtg 144
Val Ser Ser Leu Leu Tyr Val Val Tyr Ser Ile Thr Val Asn Leu Val
35 40 45

gtc acc gtg ctg ttt ccc ttg agc ttg ctg gcc agg ctg ctg ttc acc 192
Val Thr Val Leu Phe Pro Leu Ser Leu Leu Ala Arg Leu Leu Phe Thr
50 55 60

acc aac atg gcc gga ttg tgc gag aac ctg acc ata act att acc gat 240
Thr Asn Met Ala Gly Leu Cys Glu Asn Leu Thr Ile Thr Ile Thr Asp
65 70 75 80

att gtg gcc aat ttg aag ttt gcg aat gtg tac atg gtg agg aag cag 288
Ile Val Ala Asn Leu Lys Phe Ala Asn Val Tyr Met Val Arg Lys Gln
85 90 95

ctc cat gag att cgc tct ctc cta agg ctc atg gac gct aga gcc cgg 336
Leu His Glu Ile Arg Ser Leu Leu Arg Leu Met Asp Ala Arg Ala Arg
100 105 110

ctg gtg ggc gat ccc gag gag att tct gcc ttg agg aag gaa gtg aat 384
Leu Val Gly Asp Pro Glu Glu Ile Ser Ala Leu Arg Lys Glu Val Asn

115					120					125					
atc gca cag ggc act ttc cgc acc ttt gcc agt att ttc gta ttt ggc	432														
Ile Ala Gln Gly Thr Phe Arg Thr Phe Ala Ser Ile Phe Val Phe Gly															
130 135 140															
act act ttg agt tgc gtc cgc gtg gtc gtt cgc cca gat cga gag ctc	480														
Thr Thr Leu Ser Cys Val Arg Val Val Val Arg Pro Asp Arg Glu Leu															
145 150 155 160															
ctg tat ccg gcc tgg ttc ggc gtt gac tgg atg cac tcc acc aga aac	528														
Leu Tyr Pro Ala Trp Phe Gly Val Asp Trp Met His Ser Thr Arg Asn															
165 170 175															
tat gtg ctc atc aat atc tac cag ctc ttc gcc ttg ata gtg cag gct	576														
Tyr Val Leu Ile Asn Ile Tyr Gln Leu Phe Gly Leu Ile Val Gln Ala															
180 185 190															
ata cag aac tgc gct agt gac tcc tat ccg cct gcg ttt ctc tgc ctg	624														
Ile Gln Asn Cys Ala Ser Asp Ser Tyr Pro Pro Ala Phe Leu Cys Leu															
195 200 205															
ctc acg ggt cat atg cgt gct ttg gag ctg agg gtg cgg cgg att ggc	672														
Leu Thr Gly His Met Arg Ala Leu Glu Leu Arg Val Arg Arg Ile Gly															
210 215 220															
tgc agg acg gaa aag tcc aat aaa ggg cag aca tat gaa gcc tgg cgg	720														
Cys Arg Thr Glu Lys Ser Asn Lys Gly Gln Thr Tyr Glu Ala Trp Arg															
225 230 235 240															
gag gag gtg tac cag gaa ctc atc gag tgc atc cgc gat ctg gcg cgg	768														
Glu Glu Val Tyr Gln Glu Leu Ile Glu Cys Ile Arg Asp Leu Ala Arg															
245 250 255															
gtc cat cgg ctg agg gag atc att cag cgg gtc ctt tca gtg ccc tgc	816														
Val His Arg Leu Arg Glu Ile Ile Gln Arg Val Leu Ser Val Pro Cys															
260 265 270															
atg gcc cag ttc gtc tgc tcc gcc gcc gtc cag tgt acc gtc gcc atg	864														
Met Ala Gln Phe Val Cys Ser Ala Ala Val Gln Cys Thr Val Ala Met															
275 280 285															
cac ttc ctg tac gta gcg gat gac cac gac cac acc gcc atg atc atc	912														
His Phe Leu Tyr Val Ala Asp Asp His Asp His Thr Ala Met Ile Ile															
290 295 300															
tcg att gta ttt ttc tcg gcc gtc acc ttg gag gtg ttt gta atc tgc	960														
Ser Ile Val Phe Phe Ser Ala Val Thr Leu Glu Val Phe Val Ile Cys															

100	105	110
Leu Val Gly Asp Pro Glu Glu Ile Ser Ala Leu Arg Lys Glu Val Asn 115 120 125		
Ile Ala Gln Gly Thr Phe Arg Thr Phe Ala Ser Ile Phe Val Phe Gly 130 135 140		
Thr Thr Leu Ser Cys Val Arg Val Val Val Arg Pro Asp Arg Glu Leu 145 150 155 160		
Leu Tyr Pro Ala Trp Phe Gly Val Asp Trp Met His Ser Thr Arg Asn 165 170 175		
Tyr Val Leu Ile Asn Ile Tyr Gln Leu Phe Gly Leu Ile Val Gln Ala 180 185 190		
Ile Gln Asn Cys Ala Ser Asp Ser Tyr Pro Pro Ala Phe Leu Cys Leu 195 200 205		
Leu Thr Gly His Met Arg Ala Leu Glu Leu Arg Val Arg Arg Ile Gly 210 215 220		
Cys Arg Thr Glu Lys Ser Asn Lys Gly Gln Thr Tyr Glu Ala Trp Arg 225 230 235 240		
Glu Glu Val Tyr Gln Glu Leu Ile Glu Cys Ile Arg Asp Leu Ala Arg 245 250 255		
Val His Arg Leu Arg Glu Ile Ile Gln Arg Val Leu Ser Val Pro Cys 260 265 270		
Met Ala Gln Phe Val Cys Ser Ala Ala Val Gln Cys Thr Val Ala Met 275 280 285		
His Phe Leu Tyr Val Ala Asp Asp His Asp His Thr Ala Met Ile Ile 290 295 300		
Ser Ile Val Phe Phe Ser Ala Val Thr Leu Glu Val Phe Val Ile Cys 305 310 315 320		
Tyr Phe Gly Asp Arg Met Arg Thr Gln Ser Glu Ala Leu Cys Asp Ala 325 330 335		
Phe Tyr Asp Cys Asn Trp Ile Glu Gln Leu Pro Lys Phe Lys Arg Glu 340 345 350		
Leu Leu Phe Thr Leu Ala Arg Thr Gln Arg Pro Ser Leu Ile Tyr Ala		

355

360

365

Gly Asn Tyr Ile Ala Leu Ser Leu Glu Thr Phe Glu Gln Gln Val Met
 370 375 380

Arg Phe Thr Tyr Ser Val Phe Thr Leu Leu Leu Arg Ala Lys
 385 390 395

<210> 31

<211> 1191

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1191)

<223> DOR 22A.1, a coding region of BDGP Clone No.
 AC004121

<400> 31

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 Met Leu Ser Lys Phe Phe Pro His Ile Lys Glu Lys Pro Leu Ser Glu
 1 5 10 15

cgg gtt aag tcc cga gat gcc ttc att tac ttg gat cgg gtg atg tgg 96
 Arg Val Lys Ser Arg Asp Ala Phe Ile Tyr Leu Asp Arg Val Met Trp
 20 25 30

tcc ttt ggc tgg aca gag cct gaa aac aaa agg tgg atc ctt cct tat 144
 Ser Phe Gly Trp Thr Glu Pro Glu Asn Lys Arg Trp Ile Leu Pro Tyr
 35 40 45

aaa ctg tgg tta gcg ttc gtg aac ata gta atg ctc atc ctt ctg ccg 192
 Lys Leu Trp Leu Ala Phe Val Asn Ile Val Met Leu Ile Leu Leu Pro
 50 55 60

atc tcg ata agc atc gag tac ctc cac cga ttt aaa acc ttc tcg gcg 240
 Ile Ser Ile Ser Ile Glu Tyr Leu His Arg Phe Lys Thr Phe Ser Ala
 65 70 75 80

ggg gag ttc ctt agt tcc ctc gag att gga gtc aac atg tac gga agc 288
 Gly Glu Phe Leu Ser Ser Leu Glu Ile Gly Val Asn Met Tyr Gly Ser
 85 90 95

tct ttt aag tgc gcc ttc acc ttg att gga ttc aag aaa aga cag gaa 336
 Ser Phe Lys Cys Ala Phe Thr Leu Ile Gly Phe Lys Lys Arg Gln Glu

60

100						105						110						
gct	aag	gtt	tta	ctg	gat	cag	ctg	gac	aag	aga	tgc	ctt	agc	gat	aag	384		
Ala	Lys	Val	Leu	Leu	Asp	Gln	Leu	Asp	Lys	Arg	Cys	Leu	Ser	Asp	Lys			
115						120						125						
gag	agg	tcc	act	gtt	cat	cgc	tat	gtc	gcc	atg	gga	aac	ttt	ttc	gat	432		
Glu	Arg	Ser	Thr	Val	His	Arg	Tyr	Val	Ala	Met	Gly	Asn	Phe	Phe	Asp			
130						135						140						
att	ttg	tat	cac	att	ttt	tac	tcc	acc	ttc	gtg	gta	atg	aac	ttc	ccg	480		
Ile	Leu	Tyr	His	Ile	Phe	Tyr	Ser	Thr	Phe	Val	Val	Met	Asn	Phe	Pro			
145						150						155						
tat	ttt	ctg	ctt	gag	aga	cgc	cat	gct	tgg	cgc	atg	tac	ttt	cca	tat	528		
Tyr	Phe	Leu	Leu	Glu	Arg	Arg	His	Ala	Trp	Arg	Met	Tyr	Phe	Pro	Tyr			
165						170						175						
atc	gat	tcc	gac	gaa	cag	ttt	tac	atc	tcc	agc	atc	gcc	gag	tgt	ttt	576		
Ile	Asp	Ser	Asp	Glu	Gln	Phe	Tyr	Ile	Ser	Ser	Ile	Ala	Glu	Cys	Phe			
180						185						190						
ctg	atg	acg	gag	gcc	atc	tac	atg	gat	ctc	tgt	acg	gac	gtg	tgt	ccc	624		
Leu	Met	Thr	Glu	Ala	Ile	Tyr	Met	Asp	Leu	Cys	Thr	Asp	Val	Cys	Pro			
195						200						205						
ttg	atc	tcc	atg	ctt	atg	gct	cga	tgc	cac	att	agc	ctc	ctg	aaa	cag	672		
Leu	Ile	Ser	Met	Leu	Met	Ala	Arg	Cys	His	Ile	Ser	Leu	Leu	Lys	Gln			
210						215						220						
cga	ctg	aga	aat	ctc	cga	tcg	aag	cca	gga	agg	acc	gaa	gat	gag	tac	720		
Arg	Leu	Arg	Asn	Leu	Arg	Ser	Lys	Pro	Gly	Arg	Thr	Glu	Asp	Glu	Tyr			
225						230						235						
ttg	gag	gag	ctc	acc	gag	tgc	att	cgg	gat	cat	cga	ttg	cta	ttg	gac	768		
Leu	Glu	Glu	Leu	Thr	Glu	Cys	Ile	Arg	Asp	His	Arg	Leu	Leu	Leu	Asp			
245						250						255						
tat	gtt	gac	gca	ttg	cga	ccc	gtc	ttt	tcg	gga	acc	att	ttt	gtg	cag	816		
Tyr	Val	Asp	Ala	Leu	Arg	Pro	Val	Phe	Ser	Gly	Thr	Ile	Phe	Val	Gln			
260						265						270						
ttc	ctc	ctg	atc	ggg	act	gta	ctg	ggg	ctc	tca	atg	ata	aat	cta	atg	864		
Phe	Leu	Leu	Ile	Gly	Thr	Val	Leu	Gly	Leu	Ser	Met	Ile	Asn	Leu	Met			
275						280						285						
ttc	ttc	tcg	aca	ttt	tgg	act	ggg	gtc	gcc	act	tgc	ctt	ttt	atg	ttc	912		
Phe	Phe	Ser	Thr	Phe	Trp	Thr	Gly	Val	Ala	Thr	Cys	Leu	Phe	Met	Phe			

0032270 "ESTC460"

290	295	300	
gac gtg tcc atg gag acg ttc ccc ttt tgc tat ttg tgc aac atg att			960
Asp Val Ser Met Glu Thr Phe Pro Phe Cys Tyr Leu Cys Asn Met Ile			
305	310	315	320
atc gat gac tgc cag gaa atg tcc aat tgc ctc ttt caa tcg gac tgg			1008
Ile Asp Asp Cys Gln Glu Met Ser Asn Cys Leu Phe Gln Ser Asp Trp			
	325	330	335
acc tct gcc gat cgt cgc tac aaa tcc acg ttg gta tac ttt ctt cac			1056
Thr Ser Ala Asp Arg Arg Tyr Lys Ser Thr Leu Val Tyr Phe Leu His			
	340	345	350
aat ctt cag caa ccc att act ctc acg gct ggt gga gtg ttt cct att			1104
Asn Leu Gln Gln Pro Ile Thr Leu Thr Ala Gly Gly Val Phe Pro Ile			
	355	360	365
tcc atg caa aca aat ttg gct atg gtg aag ctg gca ttt tct gtg gtt			1152
Ser Met Gln Thr Asn Leu Ala Met Val Lys Leu Ala Phe Ser Val Val			
	370	375	380
acg gta att aag caa ttt aac ttg gcc gaa agg ttt caa			1191
Thr Val Ile Lys Gln Phe Asn Leu Ala Glu Arg Phe Gln			
385	390	395	
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Ser Phe Gly Trp Thr Glu Pro Glu Asn Lys Arg Trp Ile Leu Pro Tyr			
35	40	45	
Lys Leu Trp Leu Ala Phe Val Asn Ile Val Met Leu Ile Leu Leu Pro			
50	55	60	
Ile Ser Ile Ser Ile Glu Tyr Leu His Arg Phe Lys Thr Phe Ser Ala			
65	70	75	80

Thr Ser Ala Asp Arg Arg Tyr Lys Ser Thr Leu Val Tyr Phe Leu His
 340 345 350

Asn Leu Gln Gln Pro Ile Thr Leu Thr Ala Gly Gly Val Phe Pro Ile
 355 360 365

Ser Met Gln Thr Asn Leu Ala Met Val Lys Leu Ala Phe Ser Val Val
 370 375 380

Thr Val Ile Lys Gln Phe Asn Leu Ala Glu Arg Phe Gln
 385 390 395

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 <212> DNA
 <213> Drosophila melanogaster

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 <223> DOR 36E.1

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gct tgg ccc ttg gcg gtt ttt cgg tta aat cac ata ttc tgg cca ttg 96
 Ala Trp Pro Leu Ala Val Phe Arg Leu Asn His Ile Phe Trp Pro Leu
 20 25 30

gat ccg agc aca ggg aaa tgg ggc cga tat ctg gac aag gtt cta gct 144
 Asp Pro Ser Thr Gly Lys Trp Gly Arg Tyr Leu Asp Lys Val Leu Ala
 35 40 45

gtt gcg atg tcc ttg gtt ttt atg caa cac aac gat gca gag ctg agg 192
 Val Ala Met Ser Leu Val Phe Met Gln His Asn Asp Ala Glu Leu Arg
 50 55 60

tac ttg cgc ttc gag gca agt aat cgg aat ttg gat gcc ttt ctc aca 240
 Tyr Leu Arg Phe Glu Ala Ser Asn Arg Asn Leu Asp Ala Phe Leu Thr
 65 70 75 80

gga atg cca acg tat tta atc ctc gtg gag gct caa ttt aga agt ctt 288
 Gly Met Pro Thr Tyr Leu Ile Leu Val Glu Ala Gln Phe Arg Ser Leu
 85 90 95

cac att cta ctg cac ttc gag aag ctt cag aag ttt tta gaa ata ttc	336
His Ile Leu Leu His Phe Glu Lys Leu Gln Lys Phe Leu Glu Ile Phe	
100 105 110	
tac gca aat att tat att gat ccc cgt aag gaa ccc gaa atg ttt cga	384
Tyr Ala Asn Ile Tyr Ile Asp Pro Arg Lys Glu Pro Glu Met Phe Arg	
115 120 125	
aaa gtg gat gga aag atg ata att aac aga tta gtt tcg gcc atg tac	432
Lys Val Asp Gly Lys Met Ile Ile Asn Arg Leu Val Ser Ala Met Tyr	
130 135 140	
ggc gca gtt atc tct ctg tat cta atc gca ccc gtt ttt tcc atc att	480
Gly Ala Val Ile Ser Leu Tyr Leu Ile Ala Pro Val Phe Ser Ile Ile	
145 150 155 160	
aac caa agc aaa gat ttt cta tac tct atg atc ttt ccg ttc gat tcg	528
Asn Gln Ser Lys Asp Phe Leu Tyr Ser Met Ile Phe Pro Phe Asp Ser	
165 170 175	
gat ccc ttg tac ata ttt gtg cca ctg ctt ttg aca aac gta tgg gtt	576
Asp Pro Leu Tyr Ile Phe Val Pro Leu Leu Leu Thr Asn Val Trp Val	
180 185 190	
ggc att gta ata gat acc atg atg ttc ggg gag acg aat ttg ttg tgt	624
Gly Ile Val Ile Asp Thr Met Met Phe Gly Glu Thr Asn Leu Leu Cys	
195 200 205	
gaa cta att gtc cac cta aat ggt agt tat atg ttg ctc aag agg gac	672
Glu Leu Ile Val His Leu Asn Gly Ser Tyr Met Leu Leu Lys Arg Asp	
210 215 220	
ttg cag ttg gcc att gaa aag ata tta gtt gca agg gac cgt ccg cat	720
Leu Gln Leu Ala Ile Glu Lys Ile Leu Val Ala Arg Asp Arg Pro His	
225 230 235 240	
atg gcc aaa cag cta aag gtt tta att aca aaa act ctc cga aag aat	768
Met Ala Lys Gln Leu Lys Val Leu Ile Thr Lys Thr Leu Arg Lys Asn	
245 250 255	
gtg gct cta aat cag ttt ggc cag cag ctg gag gct cag tat act gtg	816
Val Ala Leu Asn Gln Phe Gly Gln Gln Leu Glu Ala Gln Tyr Thr Val	
260 265 270	
cgg gtt ttt att atg ttt gca ttc gct gcg ggc ctt tta tgt gct ctt	864
Arg Val Phe Ile Met Phe Ala Phe Ala Ala Gly Leu Leu Cys Ala Leu	
275 280 285	

tct ttt aag gct tat acg acg gat tcc ctc agc aca atg tac tac ctt 912
 Ser Phe Lys Ala Tyr Thr Thr Asp Ser Leu Ser Thr Met Tyr Tyr Leu
 290 295 300

acc cat tgg gag caa atc ctg cag tac tct aca aat ccc agc gaa aat 960
 Thr His Trp Glu Gln Ile Leu Gln Tyr Ser Thr Asn Pro Ser Glu Asn
 305 310 315 320

ctg cga tta cta aag ctc att aac ttg gcc att gag atg aac agc aag 1008
 Leu Arg Leu Leu Lys Leu Ile Asn Leu Ala Ile Glu Met Asn Ser Lys
 325 330 335

ccc ttc tat gtg aca ggg cta aaa tat ttt cgc gtt agt ctg cag gct 1056
 Pro Phe Tyr Val Thr Gly Leu Lys Tyr Phe Arg Val Ser Leu Gln Ala
 340 345 350

ggc tta aaa gta agt gaa aaa cga gtg caa aac cat ttc act gtc agc 1104
 Gly Leu Lys Val Ser Glu Lys Arg Val Gln Asn His Phe Thr Val Ser
 355 360 365

tct ttc aca gat tct gca ggc atc ctt ctc gta ctt cac att cct cac 1152
 Ser Phe Thr Asp Ser Ala Gly Ile Leu Leu Val Leu His Ile Pro His
 370 375 380

ttc gat gca gcg acg aca aat gag caa tta aat aat tca cat ttt ttt 1200
 Phe Asp Ala Ala Thr Thr Asn Glu Gln Leu Asn Asn Ser His Phe Phe
 385 390 395 400

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 <211> 400
 <212> PRT
 <213> Drosophila melanogaster

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 20 25 30

Asp Pro Ser Thr Gly Lys Trp Gly Arg Tyr Leu Asp Lys Val Leu Ala
 35 40 45

Val Ala Met Ser Leu Val Phe Met Gln His Asn Asp Ala Glu Leu Arg
 50 55 60

Leu Arg Leu Leu Lys Leu Ile Asn Leu Ala Ile Glu Met Asn Ser Lys
 325 330 335

Pro Phe Tyr Val Thr Gly Leu Lys Tyr Phe Arg Val Ser Leu Gln Ala
 340 345 350

Gly Leu Lys Val Ser Glu Lys Arg Val Gln Asn His Phe Thr Val Ser
 355 360 365

Ser Phe Thr Asp Ser Ala Gly Ile Leu Leu Val Leu His Ile Pro His
 370 375 380

Phe Asp Ala Ala Thr Thr Asn Glu Gln Leu Asn Asn Ser His Phe Phe
 385 390 395 400

<210> 35
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 <213> Drosophila melanogaster

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 <223> DOR 41E.1

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 1 5 10 15

tcc cga gat ggt tgc atc tac ctt tac cgc gcc atg aag ttt att gga 96
 Ser Arg Asp Gly Cys Ile Tyr Leu Tyr Arg Ala Met Lys Phe Ile Gly
 20 25 30

tgg ctg ccc ccc aag cag ggt gtg ctc cgg tat gtg tac ctc acc tgg 144
 Trp Leu Pro Pro Lys Gln Gly Val Leu Arg Tyr Val Tyr Leu Thr Trp
 35 40 45

acg cta atg acg ttc gtg tgg tgt aca acg tac ctg ccg ctt ggc ttc 192
 Thr Leu Met Thr Phe Val Trp Cys Thr Thr Tyr Leu Pro Leu Gly Phe
 50 55 60

ctt ggt agc tac atg acg cag atc aag tcc ttc tcc cct gga gag ttt 240
 Leu Gly Ser Tyr Met Thr Gln Ile Lys Ser Phe Ser Pro Gly Glu Phe
 65 70 75 80

ttt ctg ctg atc ggc ctg gtt ctg ggc ttc acg ctg atc aac gtg ttt 864
Phe Leu Leu Ile Gly Leu Val Leu Gly Phe Thr Leu Ile Asn Val Phe
275 280 285

ttc ttc tca gac atc tgg acg ggc atc gca tca ttt atg ttt gtt ata 912
Phe Phe Ser Asp Ile Trp Thr Gly Ile Ala Ser Phe Met Phe Val Ile
290 295 300

acc att ttg ctg cag acc ttc ccc ttc tgc tac aca tgc aac ctc atc 960
Thr Ile Leu Leu Gln Thr Phe Pro Phe Cys Tyr Thr Cys Asn Leu Ile
305 310 315 320

atg gag gac tgc gag tcc ttg acc cat gct att ttc cag tcc aac tgg 1008
Met Glu Asp Cys Glu Ser Leu Thr His Ala Ile Phe Gln Ser Asn Trp
325 330 335

gtg gat gcc agt cgt cgc tac aaa aca aca cta ctg tat ttt ctc caa 1056
Val Asp Ala Ser Arg Arg Tyr Lys Thr Thr Leu Leu Tyr Phe Leu Gln
340 345 350

aac gtg cag cag cct atc gtt ttc att gca ggc ggt atc ttt cag ata 1104
Asn Val Gln Gln Pro Ile Val Phe Ile Ala Gly Gly Ile Phe Gln Ile
355 360 365

tcc atg agc agc aac ata agt gtg gca aag ttt gct ttc tcc gtg ata 1152
Ser Met Ser Ser Asn Ile Ser Val Ala Lys Phe Ala Phe Ser Val Ile
370 375 380

acc att acc aag caa atg aat ata gct gac aaa ttt aag acg gac 1197
Thr Ile Thr Lys Gln Met Asn Ile Ala Asp Lys Phe Lys Thr Asp
385 390 395

<210> 36

<211> 399

<212> PRT

<213> Drosophila melanogaster

<400> 36

Met Val Phe Glu Leu Ile Arg Pro Ala Pro Leu Thr Glu Gln Lys Arg
1 5 10 15

Ser Arg Asp Gly Cys Ile Tyr Leu Tyr Arg Ala Met Lys Phe Ile Gly
20 25 30

Trp Leu Pro Pro Lys Gln Gly Val Leu Arg Tyr Val Tyr Leu Thr Trp
35 40 45

Thr Ile Leu Leu Gln Thr Phe Pro Phe Cys Tyr Thr Cys Asn Leu Ile
305 310 315 320

Met Glu Asp Cys Glu Ser Leu Thr His Ala Ile Phe Gln Ser Asn Trp
325 330 335

Val Asp Ala Ser Arg Arg Tyr Lys Thr Thr Leu Leu Tyr Phe Leu Gln
340 345 350

Asn Val Gln Gln Pro Ile Val Phe Ile Ala Gly Gly Ile Phe Gln Ile
355 360 365

Ser Met Ser Ser Asn Ile Ser Val Ala Lys Phe Ala Phe Ser Val Ile
370 375 380

Thr Ile Thr Lys Gln Met Asn Ile Ala Asp Lys Phe Lys Thr Asp
385 390 395

<210> 37
<211> 1218
<212> DNA
<213> Drosophila melanogaster

<220>
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<222> (1)..(1218)
<223> DOR 41E.2

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Met Asp Leu Arg Arg Trp Phe Pro Thr Leu Tyr Thr Gln Ser Lys Asp
1 5 10 15

tcg cca gtt cgc tcc cga gac gcg acc ctg tac ctc cta cgc tgc gtc 96
Ser Pro Val Arg Ser Arg Asp Ala Thr Leu Tyr Leu Leu Arg Cys Val
20 25 30

ttc tta atg ggc gtc cgc aag cca cct gcc aag ttt ttc gtg gcc tac 144
Phe Leu Met Gly Val Arg Lys Pro Pro Ala Lys Phe Phe Val Ala Tyr
35 40 45

gtg ctc tgg tcc ttc gca ctg aat ttc tgc tca aca ttt tat cag cca 192
Val Leu Trp Ser Phe Ala Leu Asn Phe Cys Ser Thr Phe Tyr Gln Pro
50 55 60

att ggc ttt ctc aca ggc tat ata agc cat tta tca gag ttc tcc ccg 240

Ile Gly Phe Leu Thr Gly Tyr Ile Ser His Leu Ser Glu Phe Ser Pro
65 70 75 80

gga gag ttt cta act tcg ctg cag gtg gcc ttt aat gct tgg tcc tgc 288
Gly Glu Phe Leu Thr Ser Leu Gln Val Ala Phe Asn Ala Trp Ser Cys
85 90 95

tct aca aaa gtc ctg ata gtg tgg gca cta gtt aag cgc ttt gac gag 336
Ser Thr Lys Val Leu Ile Val Trp Ala Leu Val Lys Arg Phe Asp Glu
100 105 110

gct aat aac ctt ctC gac gag atg gat agg cgt atc aca gac ccc gga 384
Ala Asn Asn Leu Leu Asp Glu Met Asp Arg Arg Ile Thr Asp Pro Gly
115 120 125

gag cgt ctt cag att cat cgc gct gtc tcc ctc agt aac cgt ata ttc 432
Glu Arg Leu Gln Ile His Arg Ala Val Ser Leu Ser Asn Arg Ile Phe
130 135 140

ttc	ttt	ttc	atg	gca	gtc	tac	atg	gtt	tat	gcc	act	aat	acg	ttt	ctg	480
Phe	Phe	Phe	Met	Ala	Val	Tyr	Met	Val	Tyr	Ala	Thr	Asn	Thr	Phe	Leu	
145					150					155					160	

tgc	gac	atc	ttc	att	gga	agg	cca	ccg	tac	caa	aat	tac	tac	cct	ttt	528
Ser	Ala	Ile	Phe	Ile	Gly	Arg	Pro	Pro	Tyr	Gln	Asn	Tyr	Tyr	Pro	Phe	
				165					170					175		

ctg gac tgg cga tct agc act ctg cat cta gct ctg cag gcc ggt ctg 576
Leu Asp Trp Arg Ser Ser Thr Leu His Leu Ala Leu Gln Ala Gly Leu
180 185 190

gaa tac ttc gcc atg gct ggc gcc tgc ttc cag gac gtt tgc gtt gat 624
Glu Tyr Phe Ala Met Ala Gly Ala Cys Phe Gln Asp Val Cys Val Asp
195 200 205

tgc	tac	cca	gtc	aat	ttc	gtt	ttg	gtc	ctg	cgt	gcc	cac	atg	tcg	atc	672
Cys	Tyr	Pro	Val	Asn	Phe	Val	Leu	Val	Leu	Arg	Ala	His	Met	Ser	Ile	
	210					215					220					

ttc gcg gag cgc ctt cga cgt ttg gga act tat cct tat gaa agc cag 720
Phe Ala Glu Arg Leu Arg Arg Leu Gly Thr Tyr Pro Tyr Glu Ser Gln
225 230 235 240

gag cag aaa tat gaa cga ttg gtt cag tgc ata caa gat cac aaa gta 768
Glu Gln Lys Tyr Glu Arg Leu Val Gln Cys Ile Gln Asp His Lys Val
245 250 255

att ttg cga ttt gtt gac tgc ctg cgt cct gtt att tct ggt acc atc 816

003270-227646

Ile Leu Arg Phe Val Asp Cys Leu Arg Pro Val Ile Ser Gly Thr Ile
260 265 270

ttc gtg caa ttc ttg gtt gtg ggg ttg gtg ctg ggc ttt acc cta att 864
Phe Val Gln Phe Leu Val Val Gly Leu Val Leu Gly Phe Thr Leu Ile
275 280 285

aac att gtc ctg ttc gcc aac ttg gga tcg gcc atc gca gcg ctc tcg 912
Asn Ile Val Leu Phe Ala Asn Leu Gly Ser Ala Ile Ala Ala Leu Ser
290 295 300

ttt atg gcc gca gtg ctt cta gag acg act ccc ttc tgc ata ttg tgc 960
Phe Met Ala Ala Val Leu Leu Glu Thr Thr Pro Phe Cys Ile Leu Cys
305 310 315 320

aat tat ctc aca gaa gac tgc tac aag ctg gcc gat gcc ctg ttt cag 1008
Asn Tyr Leu Thr Glu Asp Cys Tyr Lys Leu Ala Asp Ala Leu Phe Gln
325 330 335

tca aac tgg att gat gag gag aaa cga tac caa aag aca ctc atg tac 1056
Ser Asn Trp Ile Asp Glu Glu Lys Arg Tyr Gln Lys Thr Leu Met Tyr
340 345 350

ttc cta cag aaa ctg cag cag cct ata acc ttc atg gct atg aac gtg 1104
Phe Leu Gln Lys Leu Gln Gln Pro Ile Thr Phe Met Ala Met Asn Val
355 360 365

ttt cca ata tct gtg gga act aac atc agt gtc aca aaa ttt tcg ttc 1152
Phe Pro Ile Ser Val Gly Thr Asn Ile Ser Val Thr Lys Phe Ser Phe
370 375 380

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Ser Val Phe Thr Leu Val Lys Gln Met Asn Ile Ser Glu Lys Leu Ala
385 390 395 400

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Lys Ser Glu Met Glu Glu
405

<210> 38

<211> 406

<212> PRT

<213> Drosophila melanogaster

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005270 2256400

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275 280 285

Asn Ile Val Leu Phe Ala Asn Leu Gly Ser Ala Ile Ala Ala Leu Ser
290 295 300

Phe Met Ala Ala Val Leu Leu Glu Thr Thr Pro Phe Cys Ile Leu Cys
305 310 315 320

Asn Tyr Leu Thr Glu Asp Cys Tyr Lys Leu Ala Asp Ala Leu Phe Gln
325 330 335

Ser Asn Trp Ile Asp Glu Glu Lys Arg Tyr Gln Lys Thr Leu Met Tyr
340 345 350

Phe Leu Gln Lys Leu Gln Gln Pro Ile Thr Phe Met Ala Met Asn Val
355 360 365

Phe Pro Ile Ser Val Gly Thr Asn Ile Ser Val Thr Lys Phe Ser Phe
370 375 380

Ser Val Phe Thr Leu Val Lys Gln Met Asn Ile Ser Glu Lys Leu Ala
385 390 395 400

Lys Ser Glu Met Glu Glu
405

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<212> DNA
<213> Drosophila melanogaster

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<222> (1)..(1188)
<223> DOR 45F.1

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ttc ttc gtc acc aga tac tcc ttt ggc ctg ctg ggc ctg aga ttt ggc 96
Phe Phe Val Thr Arg Tyr Ser Phe Gly Leu Leu Gly Leu Arg Phe Gly
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aaa gag caa tcg tgg ctt cac ctc ttg tgg ctg gtg ttc aat ttc gtt	144
Lys Glu Gln Ser Trp Leu His Leu Leu Trp Leu Val Phe Asn Phe Val	
35 40 45	
aac ctg gcg cac tgc tgc cag gcg gag ttc gtc ttc ggc tgg agt cac	192
Asn Leu Ala His Cys Cys Gln Ala Glu Phe Val Phe Gly Trp Ser His	
50 55 60	
ttg cgc acc agt ccc gtg gat gcc atg gac gcc ttt tgt cct ctg gcc	240
Leu Arg Thr Ser Pro Val Asp Ala Met Asp Ala Phe Cys Pro Leu Ala	
65 70 75 80	
tgc agt ttc acc acg ctc ttc aag ctg gga tgg atg tgg tgg cgt cgc	288
Cys Ser Phe Thr Thr Leu Phe Lys Leu Gly Trp Met Trp Trp Arg Arg	
85 90 95	
cag gaa gta gct gat cta atg gac cgc atc cgc ttg ctc atc ggg gag	336
Gln Glu Val Ala Asp Leu Met Asp Arg Ile Arg Leu Leu Ile Gly Glu	
100 105 110	
cag gag aag agg gag gac tcc cgg aga aag gtg gct caa agg agc tac	384
Gln Glu Lys Arg Glu Asp Ser Arg Arg Lys Val Ala Gln Arg Ser Tyr	
115 120 125	
tat ctc atg gtc acc agg tgc ggt atg ctg gtc ttc acc ctg ggc agc	432
Tyr Leu Met Val Thr Arg Cys Gly Met Leu Val Phe Thr Leu Gly Ser	
130 135 140	
att acc act gga gcc ttc gtt ctg cgt tcc ctt tgg gaa atg tgg gtg	480
Ile Thr Thr Gly Ala Phe Val Leu Arg Ser Leu Trp Glu Met Trp Val	
145 150 155 160	
cgt cgt cat cag gag ttc aaa ttc gat atg ccc ttt cgc atg ctg ttc	528
Arg Arg His Gln Glu Phe Lys Phe Asp Met Pro Phe Arg Met Leu Phe	
165 170 175	
cac gac ttt gcg cat cgc atg ccc tgg ttt cca gtt ttc tat ctc tac	576
His Asp Phe Ala His Arg Met Pro Trp Phe Pro Val Phe Tyr Leu Tyr	
180 185 190	
tcc aca tgg agt ggc cag gtc act gtg tac gcc ttt gct ggt aca gat	624
Ser Thr Trp Ser Gly Gln Val Thr Val Tyr Ala Phe Ala Gly Thr Asp	
195 200 205	
ggt ttc ttc ttt ggc ttt acc ctc tac atg gcc ttc ttg ctg cag gcc	672
Gly Phe Phe Phe Gly Phe Thr Leu Tyr Met Ala Phe Leu Leu Gln Ala	
210 215 220	

tta aga tac gat atc cag gat gcc ctc aag cca ata aga gat ccc tcg	720
Leu Arg Tyr Asp Ile Gln Asp Ala Leu Lys Pro Ile Arg Asp Pro Ser	
225 230 235 240	
ctt agg gaa tcc aaa atc tgc tgt cag cga ttg gcg gac atc gtg gat	768
Leu Arg Glu Ser Lys Ile Cys Cys Gln Arg Leu Ala Asp Ile Val Asp	
245 250 255	
cgc cac aat gag ata gag aag ata gtc aag gaa ttt tct gga att atg	816
Arg His Asn Glu Ile Glu Lys Ile Val Lys Glu Phe Ser Gly Ile Met	
260 265 270	
gct gct cca act ttt gtt cac ttc gta tca gcc agc tta gtg ata gcc	864
Ala Ala Pro Thr Phe Val His Phe Val Ser Ala Ser Leu Val Ile Ala	
275 280 285	
acc agc gtc att gat ata cta ttg tat tcc gcc tat aac atc atc cgt	912
Thr Ser Val Ile Asp Ile Leu Leu Tyr Ser Gly Tyr Asn Ile Ile Arg	
290 295 300	
tac gtg gtg tac acc ttc acg gtt tcc tcg gcc atc ttc ctc tat tgc	960
Tyr Val Val Tyr Thr Phe Thr Val Ser Ser Ala Ile Phe Leu Tyr Cys	
305 310 315 320	
tac gga ggc aca gaa atg tca act gag agc ctt tcc ttg gga gaa gca	1008
Tyr Gly Gly Thr Glu Met Ser Thr Glu Ser Leu Ser Leu Gly Glu Ala	
325 330 335	
gcc tac agc agt gcc tgg tat act tgg gat cga gag acc cgc agg cgg	1056
Ala Tyr Ser Ser Ala Trp Tyr Thr Trp Asp Arg Glu Thr Arg Arg Arg	
340 345 350	
gtc ttt ctc att atc ctg cgt gct caa cga ccc att acg gtg agg gtg	1104
Val Phe Leu Ile Ile Leu Arg Ala Gln Arg Pro Ile Thr Val Arg Val	
355 360 365	
ccc ttt ttt gca cca tcg tta cca gtc ttc aca tcg gtc atc aag ttt	1152
Pro Phe Phe Ala Pro Ser Leu Pro Val Phe Thr Ser Val Ile Lys Phe	
370 375 380	
aca ggt tcg att gtg gca ctg gct aag acg ata ctg	1188
Thr Gly Ser Ile Val Ala Leu Ala Lys Thr Ile Leu	
385 390 395	

<210> 40
<211> 396

<212> PRT

<213> Drosophila melanogaster

<400> 40

Met Tyr Pro Arg Phe Leu Ser Arg Asn Tyr Pro Leu Ala Lys His Leu
1 5 10 15

Phe Phe Val Thr Arg Tyr Ser Phe Gly Leu Leu Gly Leu Arg Phe Gly
20 25 30

Lys Glu Gln Ser Trp Leu His Leu Leu Trp Leu Val Phe Asn Phe Val
35 40 45

Asn Leu Ala His Cys Cys Gln Ala Glu Phe Val Phe Gly Trp Ser His
50 55 60

Leu Arg Thr Ser Pro Val Asp Ala Met Asp Ala Phe Cys Pro Leu Ala
65 70 75 80

Cys Ser Phe Thr Thr Leu Phe Lys Leu Gly Trp Met Trp Trp Arg Arg
85 90 95

Gln Glu Val Ala Asp Leu Met Asp Arg Ile Arg Leu Leu Ile Gly Glu
100 105 110

Gln Glu Lys Arg Glu Asp Ser Arg Arg Lys Val Ala Gln Arg Ser Tyr
115 120 125

Tyr Leu Met Val Thr Arg Cys Gly Met Leu Val Phe Thr Leu Gly Ser
130 135 140

Ile Thr Thr Gly Ala Phe Val Leu Arg Ser Leu Trp Glu Met Trp Val
145 150 155 160

Arg Arg His Gln Glu Phe Lys Phe Asp Met Pro Phe Arg Met Leu Phe
165 170 175

His Asp Phe Ala His Arg Met Pro Trp Phe Pro Val Phe Tyr Leu Tyr
180 185 190

Ser Thr Trp Ser Gly Gln Val Thr Val Tyr Ala Phe Ala Gly Thr Asp
195 200 205

Gly Phe Phe Phe Gly Phe Thr Leu Tyr Met Ala Phe Leu Leu Gln Ala
210 215 220

Leu Arg Tyr Asp Ile Gln Asp Ala Leu Lys Pro Ile Arg Asp Pro Ser
225 230 235 240

ttc tgg gcc ctg ctc tat gac aaa aac ttg agg cgt tat gtg tgc att	96
Phe Trp Ala Leu Leu Tyr Asp Lys Asn Leu Arg Arg Tyr Val Cys Ile	
20 25 30	
gga ctg gcc tca ttc cac atc ttc acc caa atc gtc tac atg atg agt	144
Gly Leu Ala Ser Phe His Ile Phe Thr Gln Ile Val Tyr Met Met Ser	
35 40 45	
acc aat gaa gga cta acc ggg ata att cgt aac tca tat atg ctc gtc	192
Thr Asn Glu Gly Leu Thr Gly Ile Ile Arg Asn Ser Tyr Met Leu Val	
50 55 60	
ctt tgg att aat acg gtg ctg cga gct tat ctc ttg ctg gcg gat cac	240
Leu Trp Ile Asn Thr Val Leu Arg Ala Tyr Leu Leu Leu Ala Asp His	
65 70 75 80	
gac aga tat ttg gct ttg atc caa aaa cta act gag gcc tat tac gat	288
Asp Arg Tyr Leu Ala Leu Ile Gln Lys Leu Thr Glu Ala Tyr Tyr Asp	
85 90 95	
tta ctg aat ctg aac gat tgc tat ata tgc gaa ata ttg gac cag gtg	336
Leu Leu Asn Leu Asn Asp Ser Tyr Ile Ser Glu Ile Leu Asp Gln Val	
100 105 110	
aac aag gtg gga aag ttg atg gct agg ggc aat ctg ttc ttt ggc atg	384
Asn Lys Val Gly Lys Leu Met Ala Arg Gly Asn Leu Phe Phe Gly Met	
115 120 125	
ctc aca tcc atg gga ttc ggt ctg tac cca ttg tcc tcc agc gaa aga	432
Leu Thr Ser Met Gly Phe Gly Leu Tyr Pro Leu Ser Ser Ser Glu Arg	
130 135 140	
gct ctt aat ttt aaa acc cac ttt cct ttt gca gtc ctg cca ttt ggc	480
Ala Leu Asn Phe Lys Thr His Phe Pro Phe Ala Val Leu Pro Phe Gly	
145 150 155 160	
agc aaa att cct ggt cta aat gag tac gag agt ccg tac tat gag atg	528
Ser Lys Ile Pro Gly Leu Asn Glu Tyr Glu Ser Pro Tyr Tyr Glu Met	
165 170 175	
tgg tac atc ttt cag atg ctc atc acc ccg atg ggc tgt tgc atg tac	576
Trp Tyr Ile Phe Gln Met Leu Ile Thr Pro Met Gly Cys Cys Met Tyr	
180 185 190	
att ccg tac acc agt ctg att gtg ggc ttg ata atg ttc ggc att gtg	624
Ile Pro Tyr Thr Ser Leu Ile Val Gly Leu Ile Met Phe Gly Ile Val	
195 200 205	

<210> 42
 <211> 386
 <212> PRT
 <213> Drosophila melanogaster

<400> 42

Met	Phe	Glu	Asp	Ile	Gln	Leu	Ile	Tyr	Met	Asn	Ile	Lys	Ile	Leu	Arg	1	5	10	15
Phe	Trp	Ala	Leu	Leu	Tyr	Asp	Lys	Asn	Leu	Arg	Arg	Tyr	Val	Cys	Ile	20	25	30	
Gly	Leu	Ala	Ser	Phe	His	Ile	Phe	Thr	Gln	Ile	Val	Tyr	Met	Met	Ser	35	40	45	
Thr	Asn	Glu	Gly	Leu	Thr	Gly	Ile	Ile	Arg	Asn	Ser	Tyr	Met	Leu	Val	50	55	60	
Leu	Trp	Ile	Asn	Thr	Val	Leu	Arg	Ala	Tyr	Leu	Leu	Leu	Ala	Asp	His	65	70	75	80
Asp	Arg	Tyr	Leu	Ala	Leu	Ile	Gln	Lys	Leu	Thr	Glu	Ala	Tyr	Tyr	Asp	85	90	95	
Leu	Leu	Asn	Leu	Asn	Asp	Ser	Tyr	Ile	Ser	Glu	Ile	Leu	Asp	Gln	Val	100	105	110	
Asn	Lys	Val	Gly	Lys	Leu	Met	Ala	Arg	Gly	Asn	Leu	Phe	Phe	Gly	Met	115	120	125	
Leu	Thr	Ser	Met	Gly	Phe	Gly	Leu	Tyr	Pro	Leu	Ser	Ser	Ser	Glu	Arg	130	135	140	
Ala	Leu	Asn	Phe	Lys	Thr	His	Phe	Pro	Phe	Ala	Val	Leu	Pro	Phe	Gly	145	150	155	160
Ser	Lys	Ile	Pro	Gly	Leu	Asn	Glu	Tyr	Glu	Ser	Pro	Tyr	Tyr	Glu	Met	165	170	175	
Trp	Tyr	Ile	Phe	Gln	Met	Leu	Ile	Thr	Pro	Met	Gly	Cys	Cys	Met	Tyr	180	185	190	
Ile	Pro	Tyr	Thr	Ser	Leu	Ile	Val	Gly	Leu	Ile	Met	Phe	Gly	Ile	Val	195	200	205	
Arg	Cys	Lys	Ala	Leu	Gln	His	Arg	Leu	Arg	Gln	Val	Ala	Leu	Lys	His	210	215	220	

Pro Tyr Gly Asp Arg Asp Pro Arg Glu Leu Arg Glu Glu Ile Ile Ala
225 230 235 240

Cys Ile Arg Tyr Gln Gln Ser Ile Ile Glu Tyr Met Asp His Ile Asn
245 250 255

Glu Leu Thr Thr Met Met Phe Leu Phe Glu Leu Met Ala Phe Ser Ala
260 265 270

Leu Leu Cys Ala Leu Leu Phe Met Leu Ile Ile Val Ser Gly Thr Ser
275 280 285

Gln Leu Ile Ile Val Cys Met Tyr Ile Asn Met Ile Leu Ala Gln Ile
290 295 300

Leu Ala Leu Tyr Trp Tyr Ala Asn Glu Leu Arg Glu Gln Asn Leu Ala
305 310 315 320

Val Ala Thr Ala Ala Tyr Glu Thr Glu Trp Phe Thr Phe Asp Val Pro
325 330 335

Leu Arg Lys Asn Ile Leu Phe Met Met Met Arg Ala Gln Arg Pro Ala
340 345 350

Ala Ile Leu Leu Gly Asn Ile Arg Pro Ile Thr Leu Glu Leu Phe Gln
355 360 365

Asn Leu Leu Asn Thr Thr Tyr Thr Phe Phe Thr Val Leu Lys Arg Val
370 375 380

Tyr Gly
385

<210> 43

<211> 1359

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1359)

<223> DOR 56E.1

<400> 43

atg gtt aac gct aaa cag ttt aac atg ttt aaa gtt aag gat ctg ttg 48

Val	Arg	Arg	Gly	Glu	Glu	His	Pro	Ile	Leu	Leu	Phe	Gln	Leu	Phe	Pro		
	195						200					205					
ttc	gga	gaa	ctt	tgc	gat	aac	ttc	gtt	gtt	gga	tac	ttg	gga	cct	tg	672	
Phe	Gly	Glu	Leu	Cys	Asp	Asn	Phe	Val	Val	Gly	Tyr	Leu	Gly	Pro	Trp		
	210					215					220						
tat	gct	ctg	ggc	ctg	gga	atc	acg	gct	atc	cca	ttg	tg	cac	acc	ttt	720	
Tyr	Ala	Leu	Gly	Leu	Gly	Ile	Thr	Ala	Ile	Pro	Leu	Trp	His	Thr	Phe		
	225				230					235					240		
atc	act	tgc	ctc	atg	aag	tac	gta	aat	ctc	aag	ctg	caa	ata	ctc	aac	768	
Ile	Thr	Cys	Leu	Met	Lys	Tyr	Val	Asn	Leu	Lys	Leu	Gln	Ile	Leu	Asn		
				245					250					255			
aag	cga	gtg	gag	gag	atg	gat	att	acc	cga	ctt	aat	tcc	aaa	ttg	gta	816	
Lys	Arg	Val	Glu	Glu	Met	Asp	Ile	Thr	Arg	Leu	Asn	Ser	Lys	Leu	Val		
			260					265					270				
att	ggt	cgc	cta	act	gcc	agt	gag	tta	acc	ttc	tg	caa	atg	caa	ctc	864	
Ile	Gly	Arg	Leu	Thr	Ala	Ser	Glu	Leu	Thr	Phe	Trp	Gln	Met	Gln	Leu		
			275				280					285					
ttc	aag	gaa	ttt	gta	aag	gaa	cag	ctg	agg	att	cga	aaa	ttt	gtc	cag	912	
Phe	Lys	Glu	Phe	Val	Lys	Glu	Gln	Leu	Arg	Ile	Arg	Lys	Phe	Val	Gln		
	290					295				300							
gaa	cta	cag	tat	ctg	att	tgc	gtg	cct	gtg	atg	gca	gat	ttc	att	atc	960	
Glu	Leu	Gln	Tyr	Leu	Ile	Cys	Val	Pro	Val	Met	Ala	Asp	Phe	Ile	Ile		
	305				310				315					320			
ttc	tcg	gtt	ctc	att	tgc	ttt	ctc	ttt	ttt	gcc	ttg	aca	gtt	ggc	gtt	1008	
Phe	Ser	Val	Leu	Ile	Cys	Phe	Leu	Phe	Phe	Ala	Leu	Thr	Val	Gly	Val		
			325					330					335				
cca	agc	aaa	atg	gat	tac	ttc	ttc	atg	ttc	att	tac	ctt	ttt	gtg	atg	1056	
Pro	Ser	Lys	Met	Asp	Tyr	Phe	Phe	Met	Phe	Ile	Tyr	Leu	Phe	Val	Met		
			340					345				350					
gct	ggt	ata	ttg	tg	att	tat	cat	tg	cat	gcc	acg	ttg	att	gtt	gaa	1104	
Ala	Gly	Ile	Leu	Trp	Ile	Tyr	His	Trp	His	Ala	Thr	Leu	Ile	Val	Glu		
			355				360					365					
tgt	cac	gat	gaa	ctg	agc	ctt	gct	tac	ttt	tct	tgc	gga	tg	tac	aac	1152	
Cys	His	Asp	Glu	Leu	Ser	Leu	Ala	Tyr	Phe	Ser	Cys	Gly	Trp	Tyr	Asn		
		370				375					380						
ttc	gaa	atg	cct	ttg	cag	aaa	atg	ctg	gtt	ttt	atg	atg	atg	cat	gcc	1200	

125

Cys His Asp Glu Leu Ser Leu Ala Tyr Phe Ser Cys Gly Trp Tyr Asn

370

375

380

Phe Glu Met Pro Leu Gln Lys Met Leu Val Phe Met Met Met His Ala
385 390 395 400

Gln Arg Pro Met Lys Met Arg Ala Leu Leu Val Asp Leu Asn Leu Arg
405 410 415

Thr Phe Ile Asp Val Arg Leu Leu Thr Ala Asn Ser Ile Leu Asp Leu
420 425 430

Ser Asn Ser Ser Leu Ser Phe Pro Asp Trp Pro Trp Ser Leu Gln Leu
435 440 445

Leu Gln Phe Ala Ala
450

<210> 45

<211> 1278

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1) .. (1278)

<223> DOR 69F.1

<400> 45

atg cag ttg cac gac cat atg aag tac ata gac ttg ggt tgc aag atg 48
Met Gln Leu His Asp His Met Lys Tyr Ile Asp Leu Gly Cys Lys Met
1 5 10 15

gca tgc ata cca aga tat caa tgg aaa gga cgc cct act gaa aga cag 96
Ala Cys Ile Pro Arg Tyr Gln Trp Lys Gly Arg Pro Thr Glu Arg Gln
20 25 30

ttc tac gct tcg gag caa agg ata gtg ttc ctt ctt gga acc att tgc 144
Phe Tyr Ala Ser Glu Gln Arg Ile Val Phe Leu Leu Gly Thr Ile Cys
35 40 45

cag ata ttc cag att act gga gtg ctt atc tat tgg tat tgc aat ggc 192
Gln Ile Phe Gln Ile Thr Gly Val Leu Ile Tyr Trp Tyr Cys Asn Gly
50 55 60

cgt ctt gcc acg gaa acg ggc acc ttt gtg gca caa tta tct gaa atg 240
Arg Leu Ala Thr Glu Thr Gly Thr Phe Val Ala Gln Leu Ser Glu Met

89

260

265

270

ggc tct agc cta gta ggt gcc act att gcc att tgt atg tca agt gtt 864
 Gly Ser Ser Leu Val Gly Ala Thr Ile Ala Ile Cys Met Ser Ser Val
 275 280 285

tct ata atg cta ctg gac tta gca tct gcc ttc aaa tat gcc agt ggt 912
 Ser Ile Met Leu Leu Asp Leu Ala Ser Ala Phe Lys Tyr Ala Ser Gly
 290 295 300

cta gtg gca ttc gtc ctc tac aac ttt gtc atc tgc tac atg gga acc 960
 Leu Val Ala Phe Val Leu Tyr Asn Phe Val Ile Cys Tyr Met Gly Thr
 305 310 315 320

gag gtc act tta gct cgt ata aag gtc ggt aat atg ggg caa ata cga 1008
 Glu Val Thr Leu Ala Arg Ile Lys Val Gly Asn Met Gly Gln Ile Arg
 325 330 335

cag cca cgt ttt aga gca gga tgg aat ttg aga act act tta agt att 1056
 Gln Pro Arg Phe Arg Ala Gly Trp Asn Leu Arg Thr Thr Leu Ser Ile
 340 345 350

ttg aca gca ttt tgc gtc tgg cga tgt ttc cac gag gaa gat ttg tat 1104
 Leu Thr Ala Phe Cys Val Trp Arg Cys Phe His Glu Glu Asp Leu Tyr
 355 360 365

cca acg ttt cga agg gca ttc ttt ttg cta ggt aac ttt tgc ctg gct 1152
 Pro Thr Phe Arg Arg Ala Phe Phe Leu Leu Gly Asn Phe Cys Leu Ala
 370 375 380

tac caa tgt att gga gta att ata gat tgt ata gat tgg ttc ata tat 1200
 Tyr Gln Cys Ile Gly Val Ile Ile Asp Cys Ile Asp Trp Phe Ile Tyr
 385 390 395 400

gga cgg aag gcg gtg gat acc caa aga ttc gtt gct gag atc tca gag 1248
 Gly Arg Lys Ala Val Asp Thr Gln Arg Phe Val Ala Glu Ile Ser Glu
 405 410 415

gct aca ggt gct cgt cgc agt tgg att ttt 1278
 Ala Thr Gly Ala Arg Arg Ser Trp Ile Phe
 420 425

<210> 46

<211> 426

<212> PRT

<213> Drosophila melanogaster

<400> 46

Met Gln Leu His Asp His Met Lys Tyr Ile Asp Leu Gly Cys Lys Met
1 5 10 15

Ala Cys Ile Pro Arg Tyr Gln Trp Lys Gly Arg Pro Thr Glu Arg Gln
20 25 30

Phe Tyr Ala Ser Glu Gln Arg Ile Val Phe Leu Leu Gly Thr Ile Cys
35 40 45

Gln Ile Phe Gln Ile Thr Gly Val Leu Ile Tyr Trp Tyr Cys Asn Gly
50 55 60

Arg Leu Ala Thr Glu Thr Gly Thr Phe Val Ala Gln Leu Ser Glu Met
65 70 75 80

Cys Ser Ser Phe Cys Leu Thr Phe Val Gly Phe Cys Asn Val Tyr Ala
85 90 95

Ile Ser Thr Asn Arg Asn Gln Ile Glu Thr Leu Leu Glu Glu Leu His
100 105 110

Gln Ile Tyr Pro Arg Tyr Arg Lys Asn His Tyr Arg Cys Gln His Tyr
115 120 125

Phe Asp Met Ala Met Thr Ile Met Arg Ile Glu Phe Leu Phe Tyr Met
130 135 140

Ile Leu Tyr Val Tyr Tyr Asn Ser Ala Pro Leu Trp Val Leu Leu Trp
145 150 155 160

Glu His Leu His Glu Glu Tyr Asp Leu Ser Phe Lys Thr Gln Thr Asn
165 170 175

Thr Trp Phe Pro Trp Lys Val His Gly Ser Ala Leu Gly Phe Gly Met
180 185 190

Ala Val Leu Ser Ile Thr Val Gly Ser Phe Val Gly Val Gly Phe Ser
195 200 205

Ile Val Thr Gln Asn Leu Ile Cys Leu Leu Thr Phe Gln Leu Lys Leu
210 215 220

His Tyr Asp Gly Ile Ser Ser Gln Leu Val Ser Leu Asp Cys Arg Arg
225 230 235 240

Pro Gly Ala His Lys Glu Leu Ser Ile Leu Ile Ala His His Ser Arg
245 250 255

Ile Leu Gln Leu Gly Asp Gln Val Asn Asp Ile Met Asn Phe Val Phe
 260 265 270

Gly Ser Ser Leu Val Gly Ala Thr Ile Ala Ile Cys Met Ser Ser Val
 275 280 285

Ser Ile Met Leu Leu Asp Leu Ala Ser Ala Phe Lys Tyr Ala Ser Gly
 290 295 300

Leu Val Ala Phe Val Leu Tyr Asn Phe Val Ile Cys Tyr Met Gly Thr
 305 310 315 320

Glu Val Thr Leu Ala Arg Ile Lys Val Gly Asn Met Gly Gln Ile Arg
 325 330 335

Gln Pro Arg Phe Arg Ala Gly Trp Asn Leu Arg Thr Thr Leu Ser Ile
 340 345 350

Leu Thr Ala Phe Cys Val Trp Arg Cys Phe His Glu Glu Asp Leu Tyr
 355 360 365

Pro Thr Phe Arg Arg Ala Phe Phe Leu Leu Gly Asn Phe Cys Leu Ala
 370 375 380

Tyr Gln Cys Ile Gly Val Ile Ile Asp Cys Ile Asp Trp Phe Ile Tyr
 385 390 395 400

Gly Arg Lys Ala Val Asp Thr Gln Arg Phe Val Ala Glu Ile Ser Glu
 405 410 415

Ala Thr Gly Ala Arg Arg Ser Trp Ile Phe
 420 425

<210> 47
 <211> 1242
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1) .. (1242)
 <223> DOR 69F.2

<400> 47
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1				5					10					15		
gcc caa ctt ccc aga tac acg tgg aat ggc aga cga tcc ttg gaa gtt 96																
Ala	Gln	Leu	Pro	Arg	Tyr	Thr	Trp	Asn	Gly	Arg	Arg	Ser	Leu	Glu	Val	
		20						25					30			
aaa cgc aac ttg gca aaa cgc att atc ttc tgg ctt gga gca gta aat 144																
Lys	Arg	Asn	Leu	Ala	Lys	Arg	Ile	Ile	Phe	Trp	Leu	Gly	Ala	Val	Asn	
		35					40					45				
ttg gtt tat cac aat att ggc tgc gtc atg tat ggc tat ttc ggt gat 192																
Leu	Val	Tyr	His	Asn	Ile	Gly	Cys	Val	Met	Tyr	Gly	Tyr	Phe	Gly	Asp	
	50					55					60					
gga aga aca aag gat cca att gcg tat tta gct gaa ttg gca tct gtg 240																
Gly	Arg	Thr	Lys	Asp	Pro	Ile	Ala	Tyr	Leu	Ala	Glu	Leu	Ala	Ser	Val	
65					70				75					80		
gcc agc atg ctt ggt ttc acc att gtg ggc acc ctc aac ttg tgg aag 288																
Ala	Ser	Met	Leu	Gly	Phe	Thr	Ile	Val	Gly	Thr	Leu	Asn	Leu	Trp	Lys	
			85						90					95		
atg ctg agc ctt aag acc cat ttt gag aac cta cta aat gaa ttc gag 336																
Met	Leu	Ser	Leu	Lys	Thr	His	Phe	Glu	Asn	Leu	Leu	Asn	Glu	Phe	Glu	
			100					105					110			
gaa tta ttt caa cta atc aag cac agg gcg tat cgc ata cac cac tat 384																
Glu	Leu	Phe	Gln	Leu	Ile	Lys	His	Arg	Ala	Tyr	Arg	Ile	His	His	Tyr	
		115					120					125				
caa gaa aag tat acg cgt cat ata cga aat aca ttt att ttc cat acc 432																
Gln	Glu	Lys	Tyr	Thr	Arg	His	Ile	Arg	Asn	Thr	Phe	Ile	Phe	His	Thr	
	130					135					140					
tct gcc gtt gtc tac tac aac tca cta cca att ctt cta atg att cgg 480																
Ser	Ala	Val	Val	Tyr	Tyr	Asn	Ser	Leu	Pro	Ile	Leu	Leu	Met	Ile	Arg	
145				150					155					160		
gaa cat ttc tcg aac tca cag cag ttg ggc tat aga att cag agt aat 528																
Glu	His	Phe	Ser	Asn	Ser	Gln	Gln	Leu	Gly	Tyr	Arg	Ile	Gln	Ser	Asn	
			165						170				175			
acc tgg tat ccc tgg cag gtt cag gga tca att cct gga ttt ttt gct 576																
Thr	Trp	Tyr	Pro	Trp	Gln	Val	Gln	Gly	Ser	Ile	Pro	Gly	Phe	Phe	Ala	
			180				185					190				
gca gtc gcc tgt caa atc ttt tcg tgc caa acc aat atg tgc gtc aat 624																

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Ala	Val	Ala	Cys	Gln	Ile	Phe	Ser	Cys	Gln	Thr	Asn	Met	Cys	Val	Asn		
	195						200					205					
atg	ttt	atc	cag	ttt	ctg	atc	aac	ttt	ttt	ggt	atc	cag	cta	gaa	ata	672	
Met	Phe	Ile	Gln	Phe	Leu	Ile	Asn	Phe	Phe	Gly	Ile	Gln	Leu	Glu	Ile		
	210					215					220						
cac	ttc	gat	ggt	ttg	gcc	agg	cag	ctg	gag	acc	atc	gat	gcc	cgc	aat	720	
His	Phe	Asp	Gly	Leu	Ala	Arg	Gln	Leu	Glu	Thr	Ile	Asp	Ala	Arg	Asn		
225					230					235					240		
ccc	cat	gcc	aag	gat	caa	ttg	aag	tat	ctg	att	gta	tat	cac	aca	aaa	768	
Pro	His	Ala	Lys	Asp	Gln	Leu	Lys	Tyr	Leu	Ile	Val	Tyr	His	Thr	Lys		
			245						250					255			
ttg	ctt	aat	cta	gcc	gac	aga	ggt	aat	cga	tcg	ttt	aac	ttt	acg	ttt	816	
Leu	Leu	Asn	Leu	Ala	Asp	Arg	Val	Asn	Arg	Ser	Phe	Asn	Phe	Thr	Phe		
			260					265						270			
ctc	ata	agt	ctg	tcg	gta	tcc	atg	ata	tcc	aac	tgt	ttt	ctg	gca	ttt	864	
Leu	Ile	Ser	Leu	Ser	Val	Ser	Met	Ile	Ser	Asn	Cys	Phe	Leu	Ala	Phe		
			275				280							285			
tcc	atg	acc	atg	ttc	gac	ttt	ggc	acc	tct	cta	aaa	cat	tta	ctc	gga	912	
Ser	Met	Thr	Met	Phe	Asp	Phe	Gly	Thr	Ser	Leu	Lys	His	Leu	Leu	Gly		
	290					295					300						
ctt	ttg	cta	ttc	atc	aca	tat	aat	ttt	tca	atg	tgc	cgc	agt	ggt	acg	960	
Leu	Leu	Leu	Phe	Ile	Thr	Tyr	Asn	Phe	Ser	Met	Cys	Arg	Ser	Gly	Thr		
305					310					315					320		
cac	ttg	att	tta	acg	agt	ggc	aaa	gta	ttg	cca	gcg	gcc	ttt	tat	aac	1008	
His	Leu	Ile	Leu	Thr	Ser	Gly	Lys	Val	Leu	Pro	Ala	Ala	Phe	Tyr	Asn		
				325					330					335			
aat	tgg	tat	gaa	ggc	gat	ctt	ggt	tat	cga	agg	atg	ctc	ctc	atc	ctg	1056	
Asn	Trp	Tyr	Glu	Gly	Asp	Leu	Val	Tyr	Arg	Arg	Met	Leu	Leu	Ile	Leu		
			340					345						350			
atg	atg	cgt	gct	acg	aaa	cct	tat	atg	tgg	aaa	acc	tac	aag	ctg	gca	1104	
Met	Met	Arg	Ala	Thr	Lys	Pro	Tyr	Met	Trp	Lys	Thr	Tyr	Lys	Leu	Ala		
			355					360						365			
cct	gta	tcc	ata	act	aca	tat	atg	gca	gtg	agt	ttt	tcc	tta	ctt	aca	1152	
Pro	Val	Ser	Ile	Thr	Thr	Tyr	Met	Ala	Val	Ser	Phe	Ser	Leu	Leu	Thr		
			370					375						380			
tgg	cat	tta	tta	ttc	aat	ttt	aat	tca	tgt	ggt	ggc	ttt	cag	aca	ttg	1200	

Trp His Leu Leu Phe Asn Phe Asn Ser Cys Val Gly Phe Gln Thr Leu
385 390 395 400

aag ttt tca tat caa atg ttt acc tgt gtg cgg tcc ctt aaa
Lys Phe Ser Tyr Gln Met Phe Thr Cys Val Arg Ser Leu Lys
405 410

1242

<210> 48

<211> 414

<212> PRT

<213> Drosophila melanogaster

<400> 48

Met Gln Leu Glu Asp Phe Met Arg Tyr Pro Asp Leu Val Cys Gln Ala
1 5 10 15

Ala Gln Leu Pro Arg Tyr Thr Trp Asn Gly Arg Arg Ser Leu Glu Val
20 25 30

Lys Arg Asn Leu Ala Lys Arg Ile Ile Phe Trp Leu Gly Ala Val Asn
35 40 45

Leu Val Tyr His Asn Ile Gly Cys Val Met Tyr Gly Tyr Phe Gly Asp
50 55 60

Gly Arg Thr Lys Asp Pro Ile Ala Tyr Leu Ala Glu Leu Ala Ser Val
65 70 75 80

Ala Ser Met Leu Gly Phe Thr Ile Val Gly Thr Leu Asn Leu Trp Lys
85 90 95

Met Leu Ser Leu Lys Thr His Phe Glu Asn Leu Leu Asn Glu Phe Glu
100 105 110

Glu Leu Phe Gln Leu Ile Lys His Arg Ala Tyr Arg Ile His His Tyr
115 120 125

Gln Glu Lys Tyr Thr Arg His Ile Arg Asn Thr Phe Ile Phe His Thr
130 135 140

Ser Ala Val Val Tyr Tyr Asn Ser Leu Pro Ile Leu Leu Met Ile Arg
145 150 155 160

Glu His Phe Ser Asn Ser Gln Gln Leu Gly Tyr Arg Ile Gln Ser Asn
165 170 175

Thr Trp Tyr Pro Trp Gln Val Gln Gly Ser Ile Pro Gly Phe Phe Ala

190

Lys Phe Ser Tyr Gln Met Phe Thr Cys Val Arg Ser Leu Lys
405 410

<211> 1170

168

<212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1170)
 <223> DOR 85A.1

<400> 49

atg gaa gag cta atg aag tac gct agc ttc ttt aca cag cag tgg gca	48
Met Glu Glu Leu Met Lys Tyr Ala Ser Phe Phe Thr Gln Gln Trp Ala	
1 5 10 15	
tac ggg cat ata cca atg ggt gaa gaa tcc aaa agg aac aaa ctt ata	96
Tyr Gly His Ile Pro Met Gly Glu Glu Ser Lys Arg Asn Lys Leu Ile	
20 25 30	
ttt cac ata gtt ttt tgg tcc aat gtg att aac ctg agc ttc gtt gga	144
Phe His Ile Val Phe Trp Ser Asn Val Ile Asn Leu Ser Phe Val Gly	
35 40 45	
tta ttt gag agc att tac gtt tac agt gcc ttc atg gat aat aag ttc	192
Leu Phe Glu Ser Ile Tyr Val Tyr Ser Ala Phe Met Asp Asn Lys Phe	
50 55 60	
ctg gaa gca gtc act gcg ttg tcc tac att ggc ttc gta acc gta ggc	240
Leu Glu Ala Val Thr Ala Leu Ser Tyr Ile Gly Phe Val Thr Val Gly	
65 70 75 80	
atg agc aag atg ttc ttc atc cgg tgg aag aaa acg gct ata act gaa	288
Met Ser Lys Met Phe Phe Ile Arg Trp Lys Lys Thr Ala Ile Thr Glu	
85 90 95	
ctg att aat gaa ttg aag gag atc tat ccg aat ggt ttg atc cga gag	336
Leu Ile Asn Glu Leu Lys Glu Ile Tyr Pro Asn Gly Leu Ile Arg Glu	
100 105 110	
gaa aga tac aat ctg ccg atg tat ctg ggc acc tgc tcc aga atc agc	384
Glu Arg Tyr Asn Leu Pro Met Tyr Leu Gly Thr Cys Ser Arg Ile Ser	
115 120 125	
ctt ata tat tcc ttg ctc tac tct gtt ctc atc tgg aca ttc aac ttg	432
Leu Ile Tyr Ser Leu Leu Tyr Ser Val Leu Ile Trp Thr Phe Asn Leu	
130 135 140	
ttt tgt gta atg gag tat tgg gtc tat gac aag tgg ctc aac att cga	480
Phe Cys Val Met Glu Tyr Trp Val Tyr Asp Lys Trp Leu Asn Ile Arg	
145 150 155 160	

<210> 51
 <211> 1167
 <212> DNA
 <213> Drosophila melanogaster

<220>
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 <222> (1)..(1167)
 <223> DOR 85A.3

<400> 51

atg aag ttc atg aag tac gca gtt ttc ttt tac aca tcg gtg ggc att	48
Met Lys Phe Met Lys Tyr Ala Val Phe Phe Tyr Thr Ser Val Gly Ile	
1 5 10 15	
gag ccg tat acg att gac tcg cgg tcc aaa aaa gcg agc cta tgg tca	96
Glu Pro Tyr Thr Ile Asp Ser Arg Ser Lys Lys Ala Ser Leu Trp Ser	
20 25 30	
cat ctt ctc ttc tgg gcc aat gtg atc aat tta agt gtc att gtt ttc	144
His Leu Leu Phe Trp Ala Asn Val Ile Asn Leu Ser Val Ile Val Phe	
35 40 45	
gga gag atc ctc tat ctg gga gtg gcc tat tcc gat gga aag ttc att	192
Gly Glu Ile Leu Tyr Leu Gly Val Ala Tyr Ser Asp Gly Lys Phe Ile	
50 55 60	
gat gcc gtc act gta ctg tca tat atc gga ttc gta atc gtg ggc atg	240
Asp Ala Val Thr Val Leu Ser Tyr Ile Gly Phe Val Ile Val Gly Met	
65 70 75 80	
agc aag atg ttc ttc ata tgg tgg aag aag acc gat cta agc gat ttg	288
Ser Lys Met Phe Phe Ile Trp Trp Lys Lys Thr Asp Leu Ser Asp Leu	
85 90 95	
gtt aag gaa ttg gag cac atc tat cca aat ggc aaa gct gag gag gag	336
Val Lys Glu Leu Glu His Ile Tyr Pro Asn Gly Lys Ala Glu Glu Glu	
100 105 110	
atg tat cgg ttg gat agg tat ctg cga tct tgt tca cga att agc att	384
Met Tyr Arg Leu Asp Arg Tyr Leu Arg Ser Cys Ser Arg Ile Ser Ile	
115 120 125	
acc tat gca cta ctc tac tcc gta ctc atc tgg acc ttc aat ctg ttc	432
Thr Tyr Ala Leu Leu Tyr Ser Val Leu Ile Trp Thr Phe Asn Leu Phe	
130 135 140	

130	135	140
Ser Ile Met Gln Phe Leu Val Tyr Glu Lys Leu Leu Lys Ile Arg Val		
145	150	155 160
Val Gly Gln Thr Leu Pro Tyr Leu Met Tyr Phe Pro Trp Asn Trp His		
	165	170 175
Glu Asn Trp Thr Tyr Tyr Val Leu Leu Phe Cys Gln Asn Phe Ala Gly		
	180	185 190
His Thr Ser Ala Ser Gly Gln Ile Ser Thr Asp Leu Leu Leu Cys Ala		
	195	200 205
Val Ala Thr Gln Val Val Met His Phe Asp Tyr Leu Ala Arg Val Val		
	210	215 220
Glu Lys Gln Val Leu Asp Arg Asp Trp Ser Glu Asn Ser Arg Phe Leu		
	225	230 235 240
Ala Lys Thr Val Gln Tyr His Gln Arg Ile Leu Arg Leu Met Asp Val		
	245	250 255
Leu Asn Asp Ile Phe Gly Ile Pro Leu Leu Leu Asn Phe Met Val Ser		
	260	265 270
Thr Phe Val Ile Cys Phe Val Gly Phe Gln Met Thr Val Gly Val Pro		
	275	280 285
Pro Asp Ile Met Ile Lys Leu Phe Leu Phe Leu Phe Ser Ser Leu Ser		
	290	295 300
Gln Val Tyr Leu Ile Cys His Tyr Gly Gln Leu Ile Ala Asp Ala Ser		
	305	310 315 320
Ser Ser Leu Ser Ile Ser Ala Tyr Lys Gln Asn Trp Gln Asn Ala Asp		
	325	330 335
Ile Arg Tyr Arg Arg Ala Leu Val Phe Phe Ile Ala Arg Pro Gln Arg		
	340	345 350
Thr Thr Tyr Leu Lys Ala Thr Ile Phe Met Asn Ile Thr Arg Ala Thr		
	355	360 365
Met Thr Asp Leu Leu Gln Val Ser Tyr Lys Phe Phe Ala Leu Leu Arg		
	370	375 380
Thr Met Tyr Ile Lys		

<210> 53
 <211> 1305
 <212> DNA
 <213> *Drosophila melanogaster*

<220>
 <221> CDS
 <222> (1)..(1305)
 <223> DOR 85B.1

<400> 53
 atg gga ctc cag ttg gcg aat ggc acg aag cca tcg ccg cgg tta ccc 48
 Met Gly Leu Gln Leu Ala Asn Gly Thr Lys Pro Ser Pro Arg Leu Pro
 1 5 10 15

aaa tgg tgg cca aag cgg ctg gaa atg att ggt aaa gtg ctg ccc aaa 96
 Lys Trp Trp Pro Lys Arg Leu Glu Met Ile Gly Lys Val Leu Pro Lys
 20 25 30

gcc tat tgt tcc atg gtg att ttc acc tcc ctg cat ttg ggt gtc ctg 144
 Ala Tyr Cys Ser Met Val Ile Phe Thr Ser Leu His Leu Gly Val Leu
 35 40 45

ttc acg aaa acc aca ctg gat gtc ctg ccg acg ggg gag ctg cag gcc 192
 Phe Thr Lys Thr Thr Leu Asp Val Leu Pro Thr Gly Glu Leu Gln Ala
 50 55 60

ata acg gat gcc ctc acc atg acc ata ata tac ttt ttc acg ggc tac 240
 Ile Thr Asp Ala Leu Thr Met Thr Ile Ile Tyr Phe Phe Thr Gly Tyr
 65 70 75 80

ggc acc atc tac tgg tgc ctg cgc tcc cgg cgc ctc ttg gcc tac atg 288
 Gly Thr Ile Tyr Trp Cys Leu Arg Ser Arg Arg Leu Leu Ala Tyr Met
 85 90 95

gag cac atg aac cgg gag tat cgc cat cat tcg ctg gcc ggg gtg acc 336
 Glu His Met Asn Arg Glu Tyr Arg His His Ser Leu Ala Gly Val Thr
 100 105 110

ttt gtg agt agc cat gcg gcc ttt agg atg tcc aga aac ttc acg gtg 384
 Phe Val Ser Ser His Ala Ala Phe Arg Met Ser Arg Asn Phe Thr Val
 115 120 125

gtg tgg ata atg tcc tgc ctg ctg ggc gtg att tcc tgg ggc gtt tcg 432

Val	Trp	Ile	Met	Ser	Cys	Leu	Leu	Gly	Val	Ile	Ser	Trp	Gly	Val	Ser		
130						135					140						
cca	ctg	atg	ctg	ggc	atc	cgg	atg	ctg	ccg	ctc	caa	tgt	tgg	tat	ccc	480	
Pro	Leu	Met	Leu	Gly	Ile	Arg	Met	Leu	Pro	Leu	Gln	Cys	Trp	Tyr	Pro		
145					150					155					160		
ttc	gac	gcc	ctg	ggg	ccc	ggc	aca	tat	acg	gcg	gtc	tat	gct	aca	caa	528	
Phe	Asp	Ala	Leu	Gly	Pro	Gly	Thr	Tyr	Thr	Ala	Val	Tyr	Ala	Thr	Gln		
				165					170					175			
ctt	ttc	ggg	cag	atc	atg	gtg	ggc	atg	acc	ttt	gga	ttc	ggg	gga	tca	576	
Leu	Phe	Gly	Gln	Ile	Met	Val	Gly	Met	Thr	Phe	Gly	Phe	Gly	Gly	Ser		
			180					185						190			
ctg	ttt	gtc	acc	ctg	agc	ctg	cta	ctc	ctg	gga	caa	ttc	gat	gtg	ctc	624	
Leu	Phe	Val	Thr	Leu	Ser	Leu	Leu	Leu	Leu	Gly	Gln	Phe	Asp	Val	Leu		
		195					200						205				
tac	tgc	agc	ctg	aag	aac	ctg	gat	gcc	cat	acc	aag	ttg	ctg	ggc	ggg	672	
Tyr	Cys	Ser	Leu	Lys	Asn	Leu	Asp	Ala	His	Thr	Lys	Leu	Leu	Gly	Gly		
	210					215					220						
gag	tct	gta	aat	ggc	ctg	agt	tcg	ctg	caa	gag	gag	ttg	ctg	ctg	ggg	720	
Glu	Ser	Val	Asn	Gly	Leu	Ser	Ser	Leu	Gln	Glu	Glu	Leu	Leu	Leu	Gly		
225					230					235					240		
gac	tcg	aag	agg	gaa	tta	aat	cag	tac	gtt	ttg	ctc	cag	gag	cat	ccg	768	
Asp	Ser	Lys	Arg	Glu	Leu	Asn	Gln	Tyr	Val	Leu	Leu	Gln	Glu	His	Pro		
				245					250					255			
acg	gat	ctg	ctg	aga	ttg	tcg	gca	gga	cga	aaa	tgt	cct	gac	caa	gga	816	
Thr	Asp	Leu	Leu	Arg	Leu	Ser	Ala	Gly	Arg	Lys	Cys	Pro	Asp	Gln	Gly		
				260				265						270			
aat	gcg	ttt	cac	aac	gcc	ttg	gtg	gaa	tgc	att	cgc	ttg	cat	cgc	ttc	864	
Asn	Ala	Phe	His	Asn	Ala	Leu	Val	Glu	Cys	Ile	Arg	Leu	His	Arg	Phe		
		275					280						285				
att	ctg	cac	tgc	tca	cag	gag	ttg	gag	aat	cta	ttc	agt	cca	tat	tgt	912	
Ile	Leu	His	Cys	Ser	Gln	Glu	Leu	Glu	Asn	Leu	Phe	Ser	Pro	Tyr	Cys		
	290					295					300						
ctg	gtc	aag	tca	ctg	cag	atc	acc	ttt	cag	ctt	tgc	ctg	ctg	gtc	ttt	960	
Leu	Val	Lys	Ser	Leu	Gln	Ile	Thr	Phe	Gln	Leu	Cys	Leu	Leu	Val	Phe		
305					310					315					320		
gtg	ggc	gtt	tcg	ggg	act	cga	gag	gtc	ctg	cgg	att	gtc	aac	cag	cta	1008	

GenBank

Val Gly Val Ser Gly Thr Arg Glu Val Leu Arg Ile Val Asn Gln Leu	
325 330 335	
cag tac ttg gga ctg acc atc ttc gag ctc cta atg ttc acc tat tgt	1056
Gln Tyr Leu Gly Leu Thr Ile Phe Glu Leu Leu Met Phe Thr Tyr Cys	
340 345 350	
ggc gaa ctc ctc agt cgg cat agt att cga tct ggc gac gcc ttt tgg	1104
Gly Glu Leu Leu Ser Arg His Ser Ile Arg Ser Gly Asp Ala Phe Trp	
355 360 365	
agg ggt gcg tgg tgg aag cac gcc cat ttc atc cgc cag gac atc ctc	1152
Arg Gly Ala Trp Trp Lys His Ala His Phe Ile Arg Gln Asp Ile Leu	
370 375 380	
atc ttt ctg gtc aat agt aga cgt gca gtt cac gtg act gcc ggc aag	1200
Ile Phe Leu Val Asn Ser Arg Arg Ala Val His Val Thr Ala Gly Lys	
385 390 395 400	
ttt tat gtg atg gat gtg aat cgt cta aga tcg gtt ata acg cag gcg	1248
Phe Tyr Val Met Asp Val Asn Arg Leu Arg Ser Val Ile Thr Gln Ala	
405 410 415	
ttc agc ttc ttg act ttg ctg caa aag ttg gct gcc aag aag acg gaa	1296
Phe Ser Phe Leu Thr Leu Leu Gln Lys Leu Ala Ala Lys Lys Thr Glu	
420 425 430	
tcg gag ctc	1305
Ser Glu Leu	
435	
<210> 54	
<211> 435	
<212> PRT	
<213> Drosophila melanogaster	
<400> 54	
Met Gly Leu Gln Leu Ala Asn Gly Thr Lys Pro Ser Pro Arg Leu Pro	
1 5 10 15	
Lys Trp Trp Pro Lys Arg Leu Glu Met Ile Gly Lys Val Leu Pro Lys	
20 25 30	
Ala Tyr Cys Ser Met Val Ile Phe Thr Ser Leu His Leu Gly Val Leu	
35 40 45	
Phe Thr Lys Thr Thr Leu Asp Val Leu Pro Thr Gly Glu Leu Gln Ala	

60

Leu Val Lys Ser Leu Gln Ile Thr Phe Gln Leu Cys Leu Leu Val Phe

180

305		310		315		320
Val Gly Val Ser Gly Thr Arg Glu Val Leu Arg Ile Val Asn Gln Leu						
	325			330		335
Gln Tyr Leu Gly Leu Thr Ile Phe Glu Leu Leu Met Phe Thr Tyr Cys						
	340			345		350
Gly Glu Leu Leu Ser Arg His Ser Ile Arg Ser Gly Asp Ala Phe Trp						
	355			360		365
Arg Gly Ala Trp Trp Lys His Ala His Phe Ile Arg Gln Asp Ile Leu						
	370			375		380
Ile Phe Leu Val Asn Ser Arg Arg Ala Val His Val Thr Ala Gly Lys						
	385			390		395
Phe Tyr Val Met Asp Val Asn Arg Leu Arg Ser Val Ile Thr Gln Ala						
	405			410		415
Phe Ser Phe Leu Thr Leu Leu Gln Lys Leu Ala Ala Lys Lys Thr Glu						
	420			425		430
Ser Glu Leu						
	435					

<210> 55
 <211> 1203
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1203)

<400> 55	
atg aag cca acg gaa atc aaa aaa ccc tat cga atg gag gag ttt ctg	48
Met Lys Pro Thr Glu Ile Lys Lys Pro Tyr Arg Met Glu Glu Phe Leu	
1 5 10 15	
cgt ccg cag atg ttc cag gag gtg gct cag atg gtg cat ttc cag tgg	96
Arg Pro Gln Met Phe Gln Glu Val Ala Gln Met Val His Phe Gln Trp	
20 25 30	
cgg aga aat ccg gtg gac aac agc atg gtg aac gca tcc atg gtc ccc	144
Arg Arg Asn Pro Val Asp Asn Ser Met Val Asn Ala Ser Met Val Pro	

45

tgg	gac	atc	ata	gga	cat	ttt	tgg	ctg	gga	cat	cct	gcc	aac	cag	aat	240
Trp	Asp	Ile	Ile	Gly	His	Phe	Trp	Leu	Gly	His	Pro	Ala	Asn	Gln	Asn	
65					70					75					80	

ccg ccc gtg ctt agc atc acc att tac ttc tcg atc agg gga ttg atg 288
Pro Pro Val Leu Ser Ile Thr Ile Tyr Phe Ser Ile Arg Gly Leu Met
85 90 95

cta tac ctg aaa cga aag gaa atc gtt gag ttt gtt aac gac ttg gat 336
Leu Tyr Leu Lys Arg Lys Glu Ile Val Glu Phe Val Asn Asp Leu Asp
100 105 110

cgg gag tgt ccg cgg gac ttg gtc agc cag ttg gac atg caa atg gat 384
 Arg Glu Cys Pro Arg Asp Leu Val Ser Gln Leu Asp Met Gln Met Asp
 115 120 125

gag acg tac cga aac ttt tgg cag cgc tat cgc ttc atc cgt atc tac 432
Glu Thr Tyr Arg Asn Phe Trp Gln Arg Tyr Arg Phe Ile Arg Ile Tyr
130 135 140

tcc cat ttg ggt ggt ccg atg ttc tgc gtt gtg cca tta gct cta ttc 480
Ser His Leu Gly Gly Pro Met Phe Cys Val Val Pro Leu Ala Leu Phe
145 150 155 160

ctc ctg acc cac gag ggt aaa gat act cct gtt gcc cag cac gag cag 528
Leu Leu Thr His Glu Gly Lys Asp Thr Pro Val Ala Gln His Glu Gln
165 170 175

ctc ctt gga gga tgg ctg cca tgc ggt gtg cga aag gac cca aat ttc 576
Leu Leu Gly Gly Trp Leu Pro Cys Gly Val Arg Lys Asp Pro Asn Phe
180 185 190

tac ctt tta gtc tgg tcc ttc gac ctg atg tgc acc act tgc ggc gtc 624
Tyr Leu Leu Val Trp Ser Phe Asp Leu Met Cys Thr Thr Cys Gly Val
195 200 205

tcc ttt ttc gtt acc ttc gac aac cta ttc aat gtg atg cag gga cat 672
Ser Phe Phe Val Thr Phe Asp Asn Leu Phe Asn Val Met Gln Gly His
210 215 220

ttg gtc atg cat ttg ggc cat ctt gct cgc cag ttt tgc gcc atc gat 720
Leu Val Met His Leu Gly His Leu Ala Arg Gln Phe Ser Ala Ile Asp

<212> PRT

<213> Drosophila melanogaster

<400> 56

Met Lys Pro Thr Glu Ile Lys Lys Pro Tyr Arg Met Glu Glu Phe Leu
1 5 10 15

Arg Pro Gln Met Phe Gln Glu Val Ala Gln Met Val His Phe Gln Trp
20 25 30

Arg Arg Asn Pro Val Asp Asn Ser Met Val Asn Ala Ser Met Val Pro
35 40 45

Phe Cys Leu Ser Ala Phe Leu Asn Val Leu Phe Phe Gly Cys Asn Gly
50 55 60

Trp Asp Ile Ile Gly His Phe Trp Leu Gly His Pro Ala Asn Gln Asn
65 70 75 80

Pro Pro Val Leu Ser Ile Thr Ile Tyr Phe Ser Ile Arg Gly Leu Met
85 90 95

Leu Tyr Leu Lys Arg Lys Glu Ile Val Glu Phe Val Asn Asp Leu Asp
100 105 110

Arg Glu Cys Pro Arg Asp Leu Val Ser Gln Leu Asp Met Gln Met Asp
115 120 125

Glu Thr Tyr Arg Asn Phe Trp Gln Arg Tyr Arg Phe Ile Arg Ile Tyr
130 135 140

Ser His Leu Gly Gly Pro Met Phe Cys Val Val Pro Leu Ala Leu Phe
145 150 155 160

Leu Leu Thr His Glu Gly Lys Asp Thr Pro Val Ala Gln His Glu Gln
165 170 175

Leu Leu Gly Gly Trp Leu Pro Cys Gly Val Arg Lys Asp Pro Asn Phe
180 185 190

Tyr Leu Leu Val Trp Ser Phe Asp Leu Met Cys Thr Thr Cys Gly Val
195 200 205

Ser Phe Phe Val Thr Phe Asp Asn Leu Phe Asn Val Met Gln Gly His
210 215 220

Leu Val Met His Leu Gly His Leu Ala Arg Gln Phe Ser Ala Ile Asp
225 230 235 240

Pro Arg Gln Ser Leu Thr Asp Glu Lys Arg Phe Phe Val Asp Leu Arg
 245 250 255

Leu Leu Val Gln Arg Gln Gln Leu Leu Asn Gly Leu Cys Arg Lys Tyr
 260 265 270

Asn Asp Ile Phe Lys Val Ala Phe Leu Val Ser Asn Phe Val Gly Ala
 275 280 285

Gly Ser Leu Cys Phe Tyr Leu Phe Met Leu Ser Glu Thr Ser Asp Val
 290 295 300

Leu Ile Ile Ala Gln Tyr Ile Leu Pro Thr Leu Val Leu Val Gly Phe
 305 310 315 320

Thr Phe Glu Ile Cys Leu Arg Gly Thr Gln Leu Glu Lys Ala Ser Glu
 325 330 335

Gly Leu Glu Ser Ser Leu Arg Ser Gln Glu Trp Tyr Leu Gly Ser Arg
 340 345 350

Arg Tyr Arg Lys Phe Tyr Leu Leu Trp Thr Gln Tyr Cys Gln Arg Thr
 355 360 365

Gln Gln Leu Gly Ala Phe Gly Leu Ile Gln Val Asn Met Val His Phe
 370 375 380

Thr Glu Ile Met Gln Leu Ala Tyr Arg Leu Phe Thr Phe Leu Lys Ser
 385 390 395 400

His

<210> 57

<211> 1131

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1131)

<223> DOR 92E.1

<400> 57

atg act ttc tac aag acc atc ggc gag gat ctg tac tcc gat agg gat 48

<210> 58
 <211> 377
 <212> PRT
 <213> Drosophila melanogaster

<400> 58

Met Thr Phe Tyr Lys Thr Ile Gly Glu Asp Leu Tyr Ser Asp Arg Asp
 1 5 10 15

Pro Asn Val Ile Arg Arg Tyr Leu Leu Arg Phe Tyr Leu Val Leu Gly
 20 25 30

Phe Leu Asn Phe Asn Ala Tyr Val Val Gly Glu Ile Ala Tyr Phe Ile
 35 40 45

Val His Ile Met Ser Thr Thr Thr Leu Leu Glu Ala Thr Ala Val Ala
 50 55 60

Pro Cys Ile Gly Phe Ser Phe Met Ala Asp Phe Lys Gln Phe Gly Leu
 65 70 75 80

Thr Val Asn Arg Lys Arg Leu Val Arg Leu Leu Asp Asp Leu Lys Glu
 85 90 95

Ile Phe Pro Leu Asp Leu Glu Ala Gln Arg Lys Tyr Asn Val Ser Phe
 100 105 110

Tyr Arg Lys His Met Asn Arg Val Met Thr Leu Phe Thr Ile Leu Cys
 115 120 125

Met Thr Tyr Thr Ser Ser Phe Ser Phe Tyr Pro Ala Ile Lys Ser Thr
 130 135 140

Ile Lys Tyr Tyr Leu Met Gly Ser Glu Ile Phe Glu Arg Asn Tyr Gly
 145 150 155 160

Phe His Ile Leu Phe Pro Tyr Asp Ala Glu Thr Asp Leu Thr Val Tyr
 165 170 175

Trp Phe Ser Tyr Trp Gly Leu Ala His Cys Ala Tyr Val Ala Gly Val
 180 185 190

Ser Tyr Val Cys Val Asp Leu Leu Leu Ile Ala Thr Ile Thr Gln Leu
 195 200 205

Thr Met His Phe Asn Phe Ile Ala Asn Asp Leu Glu Ala Tyr Glu Gly
 210 215 220

<210> 60
 <211> 387
 <212> PRT
 <213> Drosophila melanogaster

<400> 60

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Val	Met	Gln	Leu	Phe	Gly	Leu	Trp	Pro	Trp	Ser	Leu	Lys	Ser	Glu	Glu
		20						25					30		
Glu	Trp	Thr	Phe	Thr	Gly	Phe	Val	Lys	Arg	Asn	Tyr	Arg	Phe	Leu	Leu
		35						40				45			
His	Leu	Pro	Ile	Thr	Phe	Thr	Phe	Ile	Gly	Leu	Met	Trp	Leu	Glu	Ala
	50						55				60				
Phe	Ile	Ser	Ser	Asn	Leu	Glu	Gln	Ala	Gly	Gln	Val	Leu	Tyr	Met	Ser
65					70					75					80
Ile	Thr	Glu	Met	Ala	Leu	Val	Val	Lys	Ile	Leu	Ser	Ile	Trp	His	Tyr
				85					90					95	
Arg	Thr	Glu	Ala	Trp	Arg	Leu	Met	Tyr	Glu	Leu	Gln	His	Ala	Pro	Asp
		100						105					110		
Tyr	Gln	Leu	His	Asn	Gln	Glu	Glu	Val	Asp	Phe	Trp	Arg	Arg	Glu	Gln
	115						120					125			
Arg	Phe	Phe	Lys	Trp	Phe	Phe	Tyr	Ile	Tyr	Ile	Leu	Ile	Ser	Leu	Gly
	130					135					140				
Val	Val	Tyr	Ser	Gly	Cys	Thr	Gly	Val	Leu	Phe	Leu	Glu	Gly	Tyr	Glu
145					150					155					160
Leu	Pro	Phe	Ala	Tyr	Tyr	Val	Pro	Phe	Glu	Trp	Gln	Asn	Glu	Arg	Arg
			165						170					175	
Tyr	Trp	Phe	Ala	Tyr	Gly	Tyr	Asp	Met	Ala	Gly	Met	Thr	Leu	Thr	Cys
		180						185					190		
Ile	Ser	Asn	Ile	Thr	Leu	Asp	Thr	Leu	Gly	Cys	Tyr	Phe	Leu	Phe	His
		195					200					205			
Ile	Ser	Leu	Leu	Tyr	Arg	Leu	Leu	Gly	Leu	Arg	Leu	Arg	Glu	Thr	Lys
	210					215					220				

Asn Met Lys Asn Asp Thr Ile Phe Gly Gln Gln Leu Arg Ala Ile Phe
225 230 235 240

Ile Met His Gln Arg Ile Arg Ser Leu Thr Leu Thr Cys Gln Arg Ile
245 250 255

Val Ser Pro Tyr Ile Leu Ser Gln Ile Ile Leu Ser Ala Leu Ile Ile
260 265 270

Cys Phe Ser Gly Tyr Arg Leu Gln His Val Gly Ile Arg Asp Asn Pro
275 280 285

Gly Gln Phe Ile Ser Met Leu Gln Phe Val Ser Val Met Ile Leu Gln
290 295 300

Ile Tyr Leu Pro Cys Tyr Tyr Gly Asn Glu Ile Thr Val Tyr Ala Asn
305 310 315 320

Gln Leu Thr Asn Glu Val Tyr His Thr Asn Trp Leu Glu Cys Arg Pro
325 330 335

Pro Ile Arg Lys Leu Leu Asn Ala Tyr Met Glu His Leu Lys Lys Pro
340 345 350

Val Thr Ile Arg Ala Gly Asn Tyr Phe Ala Val Gly Leu Pro Ile Phe
355 360 365

Val Lys Thr Ile Asn Asn Ala Tyr Ser Phe Leu Ala Leu Leu Leu Asn
370 375 380

Val Ser Asn
385

<210> 61

<211> 1101

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1101)

<400> 61

atg gag tct aca aat cgc cta agt gcc atc caa aca ctt tta gta atc 48
Met Glu Ser Thr Asn Arg Leu Ser Ala Ile Gln Thr Leu Leu Val Ile
1 5 10 15

ctt ttc agg ctt ttg gga atg cga ctg gag gcc ttg aaa aat gca gcc	672
Leu Phe Arg Leu Leu Gly Met Arg Leu Glu Ala Leu Lys Asn Ala Ala	
210 215 220	
gaa gag aaa gcc aga ccg gag ttg cgc cgc att ttc caa ctg cac act	720
Glu Glu Lys Ala Arg Pro Glu Leu Arg Arg Ile Phe Gln Leu His Thr	
225 230 235 240	
aaa gtc cgc cga ttg acg agg gaa tgc gaa gtg tta gtt tca ccc tat	768
Lys Val Arg Arg Leu Thr Arg Glu Cys Glu Val Leu Val Ser Pro Tyr	
245 250 255	
gtt cta tcc caa gtg gtc ttc agt gcc ttc atc atc tgc ttc agt gcc	816
Val Leu Ser Gln Val Val Phe Ser Ala Phe Ile Ile Cys Phe Ser Ala	
260 265 270	
tat cga ctg gtg cac atg ggc ttc aag cag cga cct gga ctc ttc gtg	864
Tyr Arg Leu Val His Met Gly Phe Lys Gln Arg Pro Gly Leu Phe Val	
275 280 285	
acc acc gtg caa ttc gtg gcc gtc atg atc gtc cag att ttc ttg ccc	912
Thr Thr Val Gln Phe Val Ala Val Met Ile Val Gln Ile Phe Leu Pro	
290 295 300	
tgt tac tac ggc aat gag ttg acc ttt cat gcc aat gca ctc act aat	960
Cys Tyr Tyr Gly Asn Glu Leu Thr Phe His Ala Asn Ala Leu Thr Asn	
305 310 315 320	
agt gtc ttc ggt acc aat tgg ctg gag tac tcc gtg ggc act cgc aag	1008
Ser Val Phe Gly Thr Asn Trp Leu Glu Tyr Ser Val Gly Thr Arg Lys	
325 330 335	
ctg ctt aac tgc tac atg gag ttc ctc aag cga ccg gtt aaa acc atc	1056
Leu Leu Asn Cys Tyr Met Glu Phe Leu Lys Arg Pro Val Lys Thr Ile	
340 345 350	
aac aat gcc tac agt ttc ttc gcc ctg ctg cta aag ata tcc aag	1101
Asn Asn Ala Tyr Ser Phe Phe Ala Leu Leu Leu Lys Ile Ser Lys	
355 360 365	

<210> 62
 <211> 367
 <212> PRT
 <213> Drosophila melanogaster

<400> 62

Met Glu Ser Thr Asn Arg Leu Ser Ala Ile Gln Thr Leu Leu Val Ile
 1 5 10 15
 Gln Arg Trp Ile Gly Leu Leu Lys Trp Glu Asn Glu Gly Glu Asp Gly
 20 25 30
 Val Leu Thr Trp Leu Lys Arg Ile Tyr Pro Phe Val Leu His Leu Pro
 35 40 45
 Leu Thr Phe Thr Tyr Ile Ala Leu Met Trp Tyr Glu Ala Ile Thr Ser
 50 55 60
 Ser Asp Phe Glu Glu Ala Gly Gln Val Leu Tyr Met Ser Ile Thr Glu
 65 70 75 80
 Leu Ala Leu Val Thr Lys Leu Leu Asn Ile Trp Tyr Arg Arg His Glu
 85 90 95
 Ala Ala Ser Leu Ile His Glu Leu Gln His Asp Pro Ala Phe Asn Leu
 100 105 110
 Arg Asn Ser Glu Glu Ile Lys Phe Trp Gln Gln Asn Gln Arg Asn Phe
 115 120 125
 Lys Arg Ile Phe Tyr Trp Tyr Ile Trp Gly Ser Leu Phe Val Ala Val
 130 135 140
 Met Gly Tyr Ile Ser Val Phe Phe Gln Glu Asp Tyr Glu Leu Pro Phe
 145 150 155 160
 Gly Tyr Tyr Val Pro Phe Glu Trp Arg Thr Arg Glu Arg Tyr Phe Tyr
 165 170 175
 Ala Trp Gly Tyr Asn Val Val Ala Met Thr Leu Cys Cys Leu Ser Asn
 180 185 190
 Ile Leu Leu Asp Thr Leu Gly Cys Tyr Phe Met Phe His Ile Ala Ser
 195 200 205
 Leu Phe Arg Leu Leu Gly Met Arg Leu Glu Ala Leu Lys Asn Ala Ala
 210 215 220
 Glu Glu Lys Ala Arg Pro Glu Leu Arg Arg Ile Phe Gln Leu His Thr
 225 230 235 240
 Lys Val Arg Arg Leu Thr Arg Glu Cys Glu Val Leu Val Ser Pro Tyr
 245 250 255

Val Leu Ser Gln Val Val Phe Ser Ala Phe Ile Ile Cys Phe Ser Ala
 260 265 270

Tyr Arg Leu Val His Met Gly Phe Lys Gln Arg Pro Gly Leu Phe Val
 275 280 285

Thr Thr Val Gln Phe Val Ala Val Met Ile Val Gln Ile Phe Leu Pro
 290 295 300

Cys Tyr Tyr Gly Asn Glu Leu Thr Phe His Ala Asn Ala Leu Thr Asn
 305 310 315 320

Ser Val Phe Gly Thr Asn Trp Leu Glu Tyr Ser Val Gly Thr Arg Lys
 325 330 335

Leu Leu Asn Cys Tyr Met Glu Phe Leu Lys Arg Pro Val Lys Thr Ile
 340 345 350

Asn Asn Ala Tyr Ser Phe Phe Ala Leu Leu Leu Lys Ile Ser Lys
 355 360 365

<210> 63

<211> 1095

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1095)

<223> DORLU 1.1

<400> 63

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 Met Trp Leu Ile Gly Trp Ile Pro Pro Lys Glu Gly Val Leu Arg Tyr
 1 5 10 15

gtg tat ctc ttc tgg acc tgc gtg ccc ttc gcc ttc ggg gtg ttt tac 96
 Val Tyr Leu Phe Trp Thr Cys Val Pro Phe Ala Phe Gly Val Phe Tyr
 20 25 30

ctg ccc gtg ggc ttc atc atc agc tac gtg cag gag ttc aag aac ttc 144
 Leu Pro Val Gly Phe Ile Ile Ser Tyr Val Gln Glu Phe Lys Asn Phe
 35 40 45

acg ccg ggc gag ttc ctt acc tcg ctg cag gtg tgc atc aat gtg tat 192
 Thr Pro Gly Glu Phe Leu Thr Ser Leu Gln Val Cys Ile Asn Val Tyr

50	55	60	
ggc gcc tcg gtg aag tcc acc atc acc tac ctc ttc ctc tgg cga ctg			240
Gly Ala Ser Val Lys Ser Thr Ile Thr Tyr Leu Phe Leu Trp Arg Leu			
65	70	75	80
cgc aag acg gag atc ctt ctg gac tcc ctg gac aag agg ctg gcg aac			288
Arg Lys Thr Glu Ile Leu Leu Asp Ser Leu Asp Lys Arg Leu Ala Asn			
	85	90	95
gac agc gat cgc gag agg atc cac aat atg gtg gcg cgc tgc aac tac			336
Asp Ser Asp Arg Glu Arg Ile His Asn Met Val Ala Arg Cys Asn Tyr			
	100	105	110
gcc ttt ctc atc tac agc ttc atc tac tgc gga tac gcg ggt tcc act			384
Ala Phe Leu Ile Tyr Ser Phe Ile Tyr Cys Gly Tyr Ala Gly Ser Thr			
	115	120	125
ttc ctg tcc tac gcc ctc agt ggt cgt cct ccg tgg tcc gtc tac aat			432
Phe Leu Ser Tyr Ala Leu Ser Gly Arg Pro Pro Trp Ser Val Tyr Asn			
	130	135	140
ccc ttc atc gat tgg cgc gat ggc atg ggc agc ctg tgg atc cag gcc			480
Pro Phe Ile Asp Trp Arg Asp Gly Met Gly Ser Leu Trp Ile Gln Ala			
	145	150	155
ata ttc gag tac atc acc atg tcc ttc gcc gtg ctg cag gac cag cta			528
Ile Phe Glu Tyr Ile Thr Met Ser Phe Ala Val Leu Gln Asp Gln Leu			
	165	170	175
tcc gac acg tat ccc ctg atg ttc acc att atg ttc ccg gcc cac atg			576
Ser Asp Thr Tyr Pro Leu Met Phe Thr Ile Met Phe Arg Ala His Met			
	180	185	190
gag gtc ctc aag gat cac gtg cgg agc ctg cgc atg gat ccc gag cgc			624
Glu Val Leu Lys Asp His Val Arg Ser Leu Arg Met Asp Pro Glu Arg			
	195	200	205
agt gag gca gac aac tat cag gat ctg gtg aac tgc gtg ctg gac cac			672
Ser Glu Ala Asp Asn Tyr Gln Asp Leu Val Asn Cys Val Leu Asp His			
	210	215	220
aag act ata ctg aaa tgc tgt gac atg att cgc ccc atg ata tcc cgc			720
Lys Thr Ile Leu Lys Cys Cys Asp Met Ile Arg Pro Met Ile Ser Arg			
	225	230	235
acc atc ttc gtg caa ttc gcg ctg att ggt tcc gtt ttg ggc ctg acc			768
Thr Ile Phe Val Gln Phe Ala Leu Ile Gly Ser Val Leu Gly Leu Thr			

Val Leu Phe Met His His Val Gln Gln Pro Ile Ile Phe Ile Ala Gly
 325 330 335

Gly Ile Phe Pro Ile Ser Met Asn Ser Asn Ile Thr Val Arg Ile Thr
 340 345 350

Ser Phe Leu Pro Thr Ala Tyr Phe Thr Phe Asp Pro Phe
 355 360 365

<210> 65

<211> 1233

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1233)

<223> DORLU 2.1

<400> 65

atg acc aag ttc ttc ttc aag cgc ctg caa act gct cca ctt gat cag 48
 Met Thr Lys Phe Phe Phe Lys Arg Leu Gln Thr Ala Pro Leu Asp Gln
 1 5 10 15

gag gtg agt tcc ctt gat gcc agc gac tac tac tac cgc atc gca ttt 96
 Glu Val Ser Ser Leu Asp Ala Ser Asp Tyr Tyr Tyr Arg Ile Ala Phe
 20 25 30

ttc ctg ggc tgg acc ccg ccc aag ggg gct ctg ctc cga tgg atc tac 144
 Phe Leu Gly Trp Thr Pro Pro Lys Gly Ala Leu Leu Arg Trp Ile Tyr
 35 40 45

tcc ctg tgg act ctg acc acg atg tgg ctg ggt atc gtg tac ctg ccg 192
 Ser Leu Trp Thr Leu Thr Thr Met Trp Leu Gly Ile Val Tyr Leu Pro
 50 55 60

ctc gga ctg agc ctc acc tat gtg aag cac ttc gat aga ttc acg ccg 240
 Leu Gly Leu Ser Leu Thr Tyr Val Lys His Phe Asp Arg Phe Thr Pro
 65 70 75 80

acg gag ttc ctg acc tcc ctg cag gtg gat atc aac tgc atc ggg aac 288
 Thr Glu Phe Leu Thr Ser Leu Gln Val Asp Ile Asn Cys Ile Gly Asn
 85 90 95

gtg atc aag tca tgc gta act tat tcc cag atg tgg cgt ttt cgc cgg 336

130

Val	Ile	Lys	Ser	Cys	Val	Thr	Tyr	Ser	Gln	Met	Trp	Arg	Phe	Arg	Arg		
			100						105					110			
atg	aat	gag	ctt	atc	tcg	tcc	ctg	gac	aag	aga	tgt	gtg	act	acg	aca	384	
Met	Asn	Glu	Leu	Ile	Ser	Ser	Leu	Asp	Lys	Arg	Cys	Val	Thr	Thr	Thr		
		115					120					125					
cag	cgt	cga	att	ttc	cat	aag	atg	gtg	gca	cgg	gtt	aat	ctc	atc	gtg	432	
Gln	Arg	Arg	Ile	Phe	His	Lys	Met	Val	Ala	Arg	Val	Asn	Leu	Ile	Val		
		130					135				140						
att	ctg	ttc	ttg	tcc	acg	tac	ttg	ggc	ttc	tgc	ttt	cta	act	ctg	ttc	480	
Ile	Leu	Phe	Leu	Ser	Thr	Tyr	Leu	Gly	Phe	Cys	Phe	Leu	Thr	Leu	Phe		
145						150				155					160		
act	tcg	gtt	ttc	gct	ggc	aaa	gct	cct	tgg	cag	ctg	tac	aac	cca	ctg	528	
Thr	Ser	Val	Phe	Ala	Gly	Lys	Ala	Pro	Trp	Gln	Leu	Tyr	Asn	Pro	Leu		
				165					170					175			
gtg	gac	tgg	cgg	aaa	ggc	cat	tgg	cag	cta	tgg	att	gcc	tcc	atc	ctg	576	
Val	Asp	Trp	Arg	Lys	Gly	His	Trp	Gln	Leu	Trp	Ile	Ala	Ser	Ile	Leu		
			180					185						190			
gag	tac	tgt	gtg	gtc	tcc	att	ggc	acc	atg	cag	gag	ttg	atg	tcc	gac	624	
Glu	Tyr	Cys	Val	Val	Ser	Ile	Gly	Thr	Met	Gln	Glu	Leu	Met	Ser	Asp		
		195					200					205					
acc	tac	gcc	ata	gtg	ttc	atc	tcc	ttg	ttc	cgc	tgc	cac	ctg	gct	att	672	
Thr	Tyr	Ala	Ile	Val	Phe	Ile	Ser	Leu	Phe	Arg	Cys	His	Leu	Ala	Ile		
		210					215				220						
ctc	aga	gat	cgc	ata	gct	aat	ctg	cgg	cag	gat	ccg	aaa	ctc	agt	gag	720	
Leu	Arg	Asp	Arg	Ile	Ala	Asn	Leu	Arg	Gln	Asp	Pro	Lys	Leu	Ser	Glu		
225					230				235						240		
atg	gaa	cac	tat	gag	cag	atg	gtg	gcc	tgc	att	cag	gat	cat	cga	acc	768	
Met	Glu	His	Tyr	Glu	Gln	Met	Val	Ala	Cys	Ile	Gln	Asp	His	Arg	Thr		
				245					250					255			
atc	ata	cag	tgc	tcc	cag	att	att	cga	ccc	atc	ctg	tcg	atc	act	atc	816	
Ile	Ile	Gln	Cys	Ser	Gln	Ile	Ile	Arg	Pro	Ile	Leu	Ser	Ile	Thr	Ile		
			260					265					270				
ttt	gcc	cag	ttc	atg	ctg	gtt	ggc	att	gac	ttg	ggt	ctg	gcg	gcc	atc	864	
Phe	Ala	Gln	Phe	Met	Leu	Val	Gly	Ile	Asp	Leu	Gly	Leu	Ala	Ala	Ile		
		275					280					285					
agc	atc	ctc	ttc	ttt	ccg	aac	acc	att	tgg	acg	atc	atg	gca	aac	gtg	912	

60

Ser Phe Ile Val Ala Ile Cys Thr Glu Ser Phe Pro Cys Cys Met Leu

204

30

Ser Val Gly Leu Leu Leu Gly Leu Ala Ala Val Ser Met Gln Phe Tyr

208

ttg att ttt gct tgg tgt gcc gta tac ttg cca atc gga atc atc att	192
Leu Ile Phe Ala Trp Cys Ala Val Tyr Leu Pro Ile Gly Ile Ile Ile	
50 55 60	
agt ttc aaa acg gat att aac aca ttc aca ccg aat gaa ctg ttg aca	240
Ser Phe Lys Thr Asp Ile Asn Thr Phe Thr Pro Asn Glu Leu Leu Thr	
65 70 75 80	
gtt atg caa tta ttt ttc aat tca gtg gga atg cca ttc aag gtt ctg	288
Val Met Gln Leu Phe Phe Asn Ser Val Gly Met Pro Phe Lys Val Leu	
85 90 95	
ttc ttc aat ttg tat att tct gga ttt tac aag gcc aaa aag ctc ctt	336
Phe Phe Asn Leu Tyr Ile Ser Gly Phe Tyr Lys Ala Lys Lys Leu Leu	
100 105 110	
agc gaa atg gac aaa cgt tgc acc act ttg aag gag cga gtg gaa gtg	384
Ser Glu Met Asp Lys Arg Cys Thr Thr Leu Lys Glu Arg Val Glu Val	
115 120 125	
cac caa ggt gtg gtc cgt tgc aac aag gcc tac ctc att tac cag ttc	432
His Gln Gly Val Val Arg Cys Asn Lys Ala Tyr Leu Ile Tyr Gln Phe	
130 135 140	
att tat acc gcg tac act att tca aca ttt cta tcg gcg gct ctt agt	480
Ile Tyr Thr Ala Tyr Thr Ile Ser Thr Phe Leu Ser Ala Ala Leu Ser	
145 150 155 160	
gga aaa ttg cca tgg cgc atc tat aat cct ttt gtg gat ttt cga gaa	528
Gly Lys Leu Pro Trp Arg Ile Tyr Asn Pro Phe Val Asp Phe Arg Glu	
165 170 175	
agt aga tcc agt ttt tgg aaa gct gcc ctc aac gag aca gca ctt atg	576
Ser Arg Ser Ser Phe Trp Lys Ala Ala Leu Asn Glu Thr Ala Leu Met	
180 185 190	
cta ttt gct gtg act caa acc cta atg agt gat ata tat cca ctg ctt	624
Leu Phe Ala Val Thr Gln Thr Leu Met Ser Asp Ile Tyr Pro Leu Leu	
195 200 205	
tat ggt ttg atc ctg aga gtt cac ctc aaa ctt ttg cga cta aga gtg	672
Tyr Gly Leu Ile Leu Arg Val His Leu Lys Leu Leu Arg Leu Arg Val	
210 215 220	
gag agc ctg tgc aca gat tct gga aaa agc gat gct gaa aac gag caa	720
Glu Ser Leu Cys Thr Asp Ser Gly Lys Ser Asp Ala Glu Asn Glu Gln	
225 230 235 240	

gat ttg att aag tgc atc aag gat cac aat ctc att att gac tat gct	768
Asp Leu Ile Lys Cys Ile Lys Asp His Asn Leu Ile Ile Asp Tyr Ala	
245 250 255	
gca gca ata cga cca gcg gtt acc cgc aca att ttc gtt caa ttc ctc	816
Ala Ala Ile Arg Pro Ala Val Thr Arg Thr Ile Phe Val Gln Phe Leu	
260 265 270	
ttg atc gga att tgc ctt ggc ctt tca atg atc aat cta ctc ttc ttt	864
Leu Ile Gly Ile Cys Leu Gly Leu Ser Met Ile Asn Leu Leu Phe Phe	
275 280 285	
gcc gac atc tgg aca gga ttg gcc aca gtg gct tac atc aat ggt cta	912
Ala Asp Ile Trp Thr Gly Leu Ala Thr Val Ala Tyr Ile Asn Gly Leu	
290 295 300	
atg gtg cag aca ttt cca ttt tgc ttc gtt tgt gat cta ctc aaa aag	960
Met Val Gln Thr Phe Pro Phe Cys Phe Val Cys Asp Leu Leu Lys Lys	
305 310 315 320	
gat tgt gaa ctt ctt gtg tcg gcc ata ttt cat tcc aac tgg att aat	1008
Asp Cys Glu Leu Leu Val Ser Ala Ile Phe His Ser Asn Trp Ile Asn	
325 330 335	
tca agc cgc agt tac aag tca tct ttg aga tat ttt ctg aag aac gcc	1056
Ser Ser Arg Ser Tyr Lys Ser Ser Leu Arg Tyr Phe Leu Lys Asn Ala	
340 345 350	
cag aaa tca att gct ttt aca gcc ggc tct att ttt ccc att tct act	1104
Gln Lys Ser Ile Ala Phe Thr Ala Gly Ser Ile Phe Pro Ile Ser Thr	
355 360 365	
ggc tcg aat att aag gtg gct aag ctg gca ttt tcg gtg gtt act ttt	1152
Gly Ser Asn Ile Lys Val Ala Lys Leu Ala Phe Ser Val Val Thr Phe	
370 375 380	
gtc aat caa ctt aac ata gct gac aga ttg aca aag aac	1191
Val Asn Gln Leu Asn Ile Ala Asp Arg Leu Thr Lys Asn	
385 390 395	

<210> 70

<211> 397

<212> PRT

<213> Drosophila melanogaster

<400> 70

Met Leu Phe Asn Tyr Leu Arg Lys Pro Asn Pro Thr Asn Leu Leu Thr

15

Ala Ala Ile Arg Pro Ala Val Thr Arg Thr Ile Phe Val Gln Phe Leu

00527-03706

260

265

270

Leu Ile Gly Ile Cys Leu Gly Leu Ser Met Ile Asn Leu Leu Phe Phe
275 280 285

Ala Asp Ile Trp Thr Gly Leu Ala Thr Val Ala Tyr Ile Asn Gly Leu
290 295 300

Met Val Gln Thr Phe Pro Phe Cys Phe Val Cys Asp Leu Leu Lys Lys
305 310 315 320

Asp Cys Glu Leu Leu Val Ser Ala Ile Phe His Ser Asn Trp Ile Asn
325 330 335

Ser Ser Arg Ser Tyr Lys Ser Ser Leu Arg Tyr Phe Leu Lys Asn Ala
340 345 350

Gln Lys Ser Ile Ala Phe Thr Ala Gly Ser Ile Phe Pro Ile Ser Thr
355 360 365

Gly Ser Asn Ile Lys Val Ala Lys Leu Ala Phe Ser Val Val Thr Phe
370 375 380

Val Asn Gln Leu Asn Ile Ala Asp Arg Leu Thr Lys Asn
385 390 395

<210> 71

<211> 1239

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1239)

<223> DORLU 6.1

<400> 71

atg gcg gtg agc act cgt gtg gcc aca aag cag gaa gtg ccc gaa tcc 48
Met Ala Val Ser Thr Arg Val Ala Thr Lys Gln Glu Val Pro Glu Ser
1 5 10 15

cgg cga gcg ttt agg aat ctc ttc aat tgc ttc tat gcc ctt ggc atg 96
Arg Arg Ala Phe Arg Asn Leu Phe Asn Cys Phe Tyr Ala Leu Gly Met
20 25 30

cag gca ccg gat ggc agt cga ccg acc acg agc agc aca tgg caa cgc 144

<210> 72
 <211> 413
 <212> PRT
 <213> Drosophila melanogaster

<400> 72

Met Ala Val Ser Thr Arg Val Ala Thr Lys Gln Glu Val Pro Glu Ser
 1 5 10 15

Arg Arg Ala Phe Arg Asn Leu Phe Asn Cys Phe Tyr Ala Leu Gly Met
 20 25 30

Gln Ala Pro Asp Gly Ser Arg Pro Thr Thr Ser Ser Thr Trp Gln Arg
 35 40 45

Ile Tyr Ala Cys Phe Ser Val Val Met Tyr Val Trp Gln Leu Leu Leu
 50 55 60

Val Pro Thr Phe Phe Val Ile Ser Tyr Arg Tyr Met Gly Gly Met Glu
 65 70 75 80

Ile Thr Gln Val Leu Thr Ser Ala Gln Val Ala Ile Asp Ala Val Ile
 85 90 95

Leu Pro Ala Lys Ile Val Ala Leu Ala Trp Asn Leu Pro Leu Leu Arg
 100 105 110

Arg Ala Glu His His Leu Ala Ala Leu Asp Ala Arg Cys Arg Glu Gln
 115 120 125

Glu Glu Phe Gln Leu Ile Leu Asp Ala Val Arg Phe Cys Asn Tyr Leu
 130 135 140

Val Trp Phe Tyr Gln Ile Cys Tyr Ala Ile Tyr Ser Ser Ser Thr Phe
 145 150 155 160

Val Cys Ala Phe Leu Leu Gly Gln Pro Pro Tyr Ala Leu Tyr Leu Pro
 165 170 175

Gly Leu Asp Trp Gln Arg Ser Gln Met Gln Phe Cys Ile Gln Ala Trp
 180 185 190

Ile Glu Phe Leu Ile Met Asn Trp Thr Cys Leu His Gln Ala Ser Asp
 195 200 205

Asp Val Tyr Ala Val Ile Tyr Leu Tyr Val Val Arg Ile Gln Val Gln
 210 215 220

Leu Leu Ala Arg Arg Val Glu Lys Leu Gly Thr Asp Asp Ser Gly Gln
 225 230 235 240
 Val Glu Ile Tyr Pro Asp Glu Arg Arg Gln Glu Glu His Cys Ala Glu
 245 250 255
 Leu Gln Arg Cys Ile Val Asp His Gln Thr Met Leu Gln Leu Leu Asp
 260 265 270
 Cys Ile Ser Pro Val Ile Ser Arg Thr Ile Phe Val Gln Phe Leu Ile
 275 280 285
 Thr Ala Ala Ile Met Gly Thr Thr Met Ile Asn Ile Phe Ile Phe Ala
 290 295 300
 Asn Thr Asn Thr Lys Ile Ala Ser Ile Ile Tyr Leu Leu Ala Val Thr
 305 310 315 320
 Leu Gln Thr Ala Pro Cys Cys Tyr Gln Ala Thr Ser Leu Met Leu Asp
 325 330 335
 Asn Glu Arg Leu Ala Leu Ala Ile Phe Gln Cys Gln Trp Leu Gly Gln
 340 345 350
 Ser Ala Arg Phe Arg Lys Met Leu Leu Tyr Tyr Leu His Arg Ala Gln
 355 360 365
 Gln Pro Ile Thr Leu Thr Ala Met Lys Leu Phe Pro Ile Asn Leu Ala
 370 375 380
 Thr Tyr Phe Ser Ile Ala Lys Phe Ser Phe Ser Leu Tyr Thr Leu Ile
 385 390 395 400
 Lys Gly Met Asn Leu Gly Glu Arg Phe Asn Arg Thr Asn
 405 410

<210> 73
 <211> 1089
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1089)
 <223> DORLU 7.1

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218

<212> PRT

<213> Drosophila melanogaster

<400> 74

Met Asp Tyr Asp Arg Ile Arg Pro Val Arg Phe Leu Thr Gly Val Leu
1 5 10 15

Lys Trp Trp Arg Leu Trp Pro Arg Lys Glu Ser Val Ser Thr Pro Asp
20 25 30

Trp Thr Asn Trp Gln Ala Tyr Ala Leu His Val Pro Phe Thr Phe Leu
35 40 45

Phe Val Leu Leu Leu Trp Leu Glu Ala Ile Lys Ser Arg Asp Ile Gln
50 55 60

His Thr Ala Asp Val Leu Leu Ile Cys Leu Thr Thr Thr Ala Leu Gly
65 70 75 80

Gly Lys Val Ile Asn Ile Trp Lys Tyr Ala His Val Ala Gln Gly Ile
85 90 95

Leu Ser Glu Trp Ser Thr Trp Asp Leu Phe Glu Leu Arg Ser Lys Gln
100 105 110

Glu Val Asp Met Trp Arg Phe Glu His Arg Arg Phe Asn Arg Val Phe
115 120 125

Met Phe Tyr Cys Leu Cys Ser Ala Gly Val Ile Pro Phe Ile Val Ile
130 135 140

Gln Pro Leu Phe Asp Ile Pro Asn Arg Leu Pro Phe Trp Met Trp Thr
145 150 155 160

Pro Phe Asp Trp Gln Gln Pro Val Leu Leu Trp Tyr Ala Phe Ile Tyr
165 170 175

Gln Ala Thr Thr Ile Pro Ile Ala Cys Ala Cys Asn Val Thr Met Asp
180 185 190

Ala Val Asn Trp Tyr Leu Met Leu His Leu Ser Leu Cys Leu Arg Met
195 200 205

Leu Gly Gln Arg Leu Ser Lys Leu Gln His Asp Asp Lys Asp Leu Arg
210 215 220

Glu Lys Phe Leu Glu Leu Ile His Leu His Gln Arg Leu Lys Gln Gln
225 230 235 240

Ala Leu Ser Ile Glu Ile Phe Ile Ser Lys Ser Thr Phe Thr Gln Ile
245 250 255

Leu Val Ser Ser Leu Ile Ile Cys Phe Thr Ile Tyr Ser Met Gln Met
260 265 270

Tyr Leu Val Ala Met Ile Met Gln Val Met Leu Pro Thr Ile Tyr Gly
275 280 285

Asn Ala Val Ile Asp Ser Ala Asn Met Leu Thr Asp Ser Met Tyr Asn
290 295 300

Ser	Asp	Trp	Pro	Asp	Met	Asn	Cys	Arg	Met	Arg	Arg	Leu	Val	Leu	Met
305					310					315					320

Phe Met Val Tyr Leu Asn Arg Pro Val Thr Leu Lys Ala Gly Gly Phe
- 325 330 335

Phe His Ile Gly Leu Pro Leu Phe Thr Lys Thr Met Asn Gln Ala Tyr
340 345 350

Ser Leu Leu Ala Leu Leu Leu Asn Met Asn Gln
355 360

<210> 75

<211> 1176

<212> DNA

<213> Drosophila melanogaster

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<221> CDS

<222> (1) .. (1176)

<223> DORLU 9.1

 $\langle 400 \rangle$ 75

atg agc gac aag gtg aag gga aaa aag cag gag gaa aag gat caa tcc 48
Met Ser Asp Lys Val Lys Gly Lys Lys Gln Glu Glu Lys Asp Gln Ser
1 5 10 15

ttg	cgg	gtg	caa	att	ctc	gtt	tat	cgc	tgc	atg	ggc	atc	gat	ttg	tgg	96
Leu	Arg	Val	Gln	Ile	Leu	Val	Tyr	Arg	Cys	Met	Gly	Ile	Asp	Leu	Trp	
			20					25					30			

agc ccc acg atg gcg aat gac cgc ccg tgg ctg acc ttt gtc aca atg 144
 Ser Pro Thr Met Ala Asn Asp Arg Pro Trp Leu Thr Phe Val Thr Met

221

35										40										45										
gga	cca	ctt	ttc	ctg	ttt	atg	gtg	ccc	atg	ttc	ctg	gcc	gcc	cac	gag	192														
Gly	Pro	Leu	Phe	Leu	Phe	Met	Val	Pro	Met	Phe	Leu	Ala	Ala	His	Glu															
50					55					60																				
tac	atc	acc	cag	gtg	agc	ctg	ctc	tcc	gac	acc	ctg	ggc	tcc	acc	ttc	240														
Tyr	Ile	Thr	Gln	Val	Ser	Leu	Leu	Ser	Asp	Thr	Leu	Gly	Ser	Thr	Phe															
65					70					75					80															
gcc	agc	atg	ctc	acc	ctg	gtc	aaa	ttc	ctg	ctc	ttc	tgc	tat	cat	cgc	288														
Ala	Ser	Met	Leu	Thr	Leu	Val	Lys	Phe	Leu	Leu	Phe	Cys	Tyr	His	Arg															
85					90					95																				
aag	gag	ttc	gtc	ggc	ctg	atc	tac	cac	atc	agg	gcc	att	ctg	gct	aaa	336														
Lys	Glu	Phe	Val	Gly	Leu	Ile	Tyr	His	Ile	Arg	Ala	Ile	Leu	Ala	Lys															
100					105					110																				
gaa	atc	gaa	gtg	tgg	cct	gat	gcg	cgg	gaa	atc	atc	gag	gtg	gag	aac	384														
Glu	Ile	Glu	Val	Trp	Pro	Asp	Ala	Arg	Glu	Ile	Ile	Glu	Val	Glu	Asn															
115					120					125																				
caa	agt	gac	caa	atg	ctc	agt	ctt	acg	tac	act	cgc	tgt	ttt	gga	ctg	432														
Gln	Ser	Asp	Gln	Met	Leu	Ser	Leu	Thr	Tyr	Thr	Arg	Cys	Phe	Gly	Leu															
130					135					140																				
gct	gga	atc	ttt	gcg	gcc	ctg	aag	ccc	ttt	gtg	ggc	atc	ata	ctc	tcc	480														
Ala	Gly	Ile	Phe	Ala	Ala	Leu	Lys	Pro	Phe	Val	Gly	Ile	Ile	Leu	Ser															
145					150					155					160															
tcg	att	cgc	ggc	gac	gag	att	cac	ctg	gag	ctg	ccc	cac	aac	ggc	gtt	528														
Ser	Ile	Arg	Gly	Asp	Glu	Ile	His	Leu	Glu	Leu	Pro	His	Asn	Gly	Val															
165					170					175																				
tac	ccg	tac	gat	ctc	cag	gtg	gtc	atg	ttt	tat	gtg	ccc	acc	tat	ctg	576														
Tyr	Pro	Tyr	Asp	Leu	Gln	Val	Val	Met	Phe	Tyr	Val	Pro	Thr	Tyr	Leu															
180					185					190																				
tgg	aat	gtg	atg	gcc	agc	tat	agt	gct	gta	acc	atg	gca	ctc	tgc	gtg	624														
Trp	Asn	Val	Met	Ala	Ser	Tyr	Ser	Ala	Val	Thr	Met	Ala	Leu	Cys	Val															
195					200					205																				
gac	tcg	ctg	ctc	ttc	ttt	ttc	acc	tac	aac	gtg	tgc	gcc	att	ttc	aag	672														
Asp	Ser	Leu	Leu	Phe	Phe	Phe	Thr	Tyr	Asn	Val	Cys	Ala	Ile	Phe	Lys															
210					215					220																				
atc	gcc	aag	cac	cgg	atg	atc	cat	ctg	ccg	gcg	gtg	ggc	gga	aag	gag	720														
Ile	Ala	Lys	His	Arg	Met	Ile	His	Leu	Pro	Ala	Val	Gly	Gly	Lys	Glu															

<400> 76

Met Ser Asp Lys Val Lys Gly Lys Lys Gln Glu Glu Lys Asp Gln Ser
1 5 10 15

Leu Arg Val Gln Ile Leu Val Tyr Arg Cys Met Gly Ile Asp Leu Trp
20 25 30

Ser Pro Thr Met Ala Asn Asp Arg Pro Trp Leu Thr Phe Val Thr Met
35 40 45

Gly Pro Leu Phe Leu Phe Met Val Pro Met Phe Leu Ala Ala His Glu
50 55 60

Tyr Ile Thr Gln Val Ser Leu Leu Ser Asp Thr Leu Gly Ser Thr Phe
65 70 75 80

Ala Ser Met Leu Thr Leu Val Lys Phe Leu Leu Phe Cys Tyr His Arg
85 90 95

Lys Glu Phe Val Gly Leu Ile Tyr His Ile Arg Ala Ile Leu Ala Lys
100 105 110

Glu Ile Glu Val Trp Pro Asp Ala Arg Glu Ile Ile Glu Val Glu Asn
115 120 125

Gln Ser Asp Gln Met Leu Ser Leu Thr Tyr Thr Arg Cys Phe Gly Leu
130 135 140

Ala Gly Ile Phe Ala Ala Leu Lys Pro Phe Val Gly Ile Ile Leu Ser
145 150 155 160

Ser Ile Arg Gly Asp Glu Ile His Leu Glu Leu Pro His Asn Gly Val
165 170 175

Tyr Pro Tyr Asp Leu Gln Val Val Met Phe Tyr Val Pro Thr Tyr Leu
180 185 190

Trp Asn Val Met Ala Ser Tyr Ser Ala Val Thr Met Ala Leu Cys Val
195 200 205

Asp Ser Leu Leu Phe Phe Phe Thr Tyr Asn Val Cys Ala Ile Phe Lys
210 215 220

Ile Ala Lys His Arg Met Ile His Leu Pro Ala Val Gly Gly Lys Glu
225 230 235 240

Glu Leu Glu Gly Leu Val Gln Val Leu Leu Leu His Gln Lys Gly Leu
245 250 255

Gln Ile Ala Asp His Ile Ala Asp Lys Tyr Arg Pro Leu Ile Phe Leu
260 265 270

Gln Phe Phe Leu Ser Ala Leu Gln Ile Cys Phe Ile Gly Phe Gln Val
275 280 285

Ala Asp Leu Phe Pro Asn Pro Gln Ser Leu Tyr Phe Ile Ala Phe Val
290 295 300

Gly Ser Leu Leu Ile Ala Leu Phe Ile Tyr Ser Lys Cys Gly Glu Asn
305 310 315 320

Ile Lys Ser Ala Ser Leu Asp Phe Gly Asn Gly Leu Tyr Glu Thr Asn
325 330 335

Trp Thr Asp Phe Ser Pro Pro Thr Lys Arg Ala Leu Leu Ile Ala Ala
340 345 350

Met Arg Ala Gln Arg Pro Cys Gln Met Lys Gly Tyr Phe Phe Glu Ala
355 360 365

Ser Met Ala Thr Phe Ser Thr Ile Val Arg Ser Ala Val Ser Tyr Ile
370 375 380

Met Met Leu Arg Ser Phe Asn Ala
385 390

<210> 77

<211> 1221

<212> DNA

<213> Drosophila melanogaster

<220>

<221> CDS

<222> (1)..(1221)

<223> DORLU 12.1

<400> 77

atg gat aac gtc gcg gaa atg cct gaa gaa aag tat gtc gaa gtc gat 48
Met Asp Asn Val Ala Glu Met Pro Glu Glu Lys Tyr Val Glu Val Asp
1 5 10 15

gat ttt ttg agg cta gct gtg aaa ttc tac aat act ttg ggc att gat 96
Asp Phe Leu Arg Leu Ala Val Lys Phe Tyr Asn Thr Leu Gly Ile Asp
20 25 30

ccc tat gaa act gga cga aaa cga act att tgg ttt caa ata tat ttc 144
Pro Tyr Glu Thr Gly Arg Lys Arg Thr Ile Trp Phe Gln Ile Tyr Phe
35 40 45

gca ttg aat atg ttt aat atg gtg ttt agt ttt tat gcc gag gta gcg 192
Ala Leu Asn Met Phe Asn Met Val Phe Ser Phe Tyr Ala Glu Val Ala
50 55 60

act ctg gtg gac agg tta cgc gat aat gaa aat ttt ctc gag agc tgc 240
Thr Leu Val Asp Arg Leu Arg Asp Asn Glu Asn Phe Leu Glu Ser Cys
65 70 75 80

atc tta ctg agc tac gtg tcc ttt gtg gtc atg ggc ctc tcc aag ata 288
Ile Leu Leu Ser Tyr Val Ser Phe Val Val Met Gly Leu Ser Lys Ile
85 90 95

ggt gct gta atg aaa aaa aag cca aaa atg aca gct ttg gtc agg caa 336
Gly Ala Val Met Lys Lys Lys Pro Lys Met Thr Ala Leu Val Arg Gln
100 105 110

ttg gag acc tgc ttt ccg tcg cca agt gca aag gtt caa gag gaa tat 384
Leu Glu Thr Cys Phe Pro Ser Pro Ser Ala Lys Val Gln Glu Glu Tyr
115 120 125

gct gtg aag tcc tgg ctg aaa cgc tgc cat ata tac aca aag gga ttt 432
Ala Val Lys Ser Trp Leu Lys Arg Cys His Ile Tyr Thr Lys Gly Phe
130 135 140

ggt ggt ctc ttc atg atc atg tat ttc gct cac gct ctg att ccc tta 480
Gly Gly Leu Phe Met Ile Met Tyr Phe Ala His Ala Leu Ile Pro Leu
145 150 155 160

ttc ata tac ttc att caa aga gtg ctg ctc cac tat ccg gat gcc aag 528
Phe Ile Tyr Phe Ile Gln Arg Val Leu Leu His Tyr Pro Asp Ala Lys
165 170 175

cag att atg ccg ttt tac caa ctc gaa cct tgg gaa ttt cgc gac tcc 576
Gln Ile Met Pro Phe Tyr Gln Leu Glu Pro Trp Glu Phe Arg Asp Ser
180 185 190

tgg ttg ttt tat cca agc tat ttt cac cag tcg tcg gcc gga tat acg 624
Trp Leu Phe Tyr Pro Ser Tyr Phe His Gln Ser Ser Ala Gly Tyr Thr
195 200 205

gct aca tgt gga tcc att gcc ggt gac cta atg atc ttc gct gtg gtc 672
Ala Thr Cys Gly Ser Ile Ala Gly Asp Leu Met Ile Phe Ala Val Val
210 215 220

<210> 78
 <211> 407
 <212> PRT
 <213> Drosophila melanogaster

<400> 78

Met Asp Asn Val Ala Glu Met Pro Glu Glu Lys Tyr Val Glu Val Asp
 1 5 10 15

Asp Phe Leu Arg Leu Ala Val Lys Phe Tyr Asn Thr Leu Gly Ile Asp
 20 25 30

Pro Tyr Glu Thr Gly Arg Lys Arg Thr Ile Trp Phe Gln Ile Tyr Phe
 35 40 45

Ala Leu Asn Met Phe Asn Met Val Phe Ser Phe Tyr Ala Glu Val Ala
 50 55 60

Thr Leu Val Asp Arg Leu Arg Asp Asn Glu Asn Phe Leu Glu Ser Cys
 65 70 75 80

Ile Leu Leu Ser Tyr Val Ser Phe Val Val Met Gly Leu Ser Lys Ile
 85 90 95

Gly Ala Val Met Lys Lys Lys Pro Lys Met Thr Ala Leu Val Arg Gln
 100 105 110

Leu Glu Thr Cys Phe Pro Ser Pro Ser Ala Lys Val Gln Glu Glu Tyr
 115 120 125

Ala Val Lys Ser Trp Leu Lys Arg Cys His Ile Tyr Thr Lys Gly Phe
 130 135 140

Gly Gly Leu Phe Met Ile Met Tyr Phe Ala His Ala Leu Ile Pro Leu
 145 150 155 160

Phe Ile Tyr Phe Ile Gln Arg Val Leu Leu His Tyr Pro Asp Ala Lys
 165 170 175

Gln Ile Met Pro Phe Tyr Gln Leu Glu Pro Trp Glu Phe Arg Asp Ser
 180 185 190

Trp Leu Phe Tyr Pro Ser Tyr Phe His Gln Ser Ser Ala Gly Tyr Thr
 195 200 205

Ala Thr Cys Gly Ser Ile Ala Gly Asp Leu Met Ile Phe Ala Val Val

157

228

210	215	220
Leu Gln Val Ile Met His Tyr Glu Arg Leu Ala Lys Val Leu Arg Glu		
225	230	235 240
Phe Lys Ile Gln Ala His Asn Ala Pro Asn Gly Ala Lys Glu Asp Ile		
245	250	255
Arg Lys Leu Gln Ser Leu Val Ala Asn His Ile Asp Ile Leu Arg Leu		
260	265	270
Thr Asp Leu Met Asn Glu Val Phe Gly Ile Pro Leu Leu Leu Asn Phe		
275	280	285
Ile Ala Ser Ala Leu Leu Val Cys Leu Val Gly Val Gln Leu Thr Ile		
290	295	300
Ala Leu Ser Pro Glu Tyr Phe Cys Lys Gln Met Leu Phe Leu Ile Ser		
305	310	315 320
Val Leu Leu Glu Val Tyr Leu Leu Cys Ser Phe Ser Gln Arg Leu Ile		
325	330	335
Asp Ala Ser Glu Asn Val Gly His Ala Ala Tyr Asp Met Asp Trp Leu		
340	345	350
Gly Ser Asp Lys Arg Phe Lys Lys Ile Leu Ile Phe Ile Ser Met Arg		
355	360	365
Ser Gln Lys Pro Val Cys Leu Lys Ala Thr Val Val Leu Asp Leu Ser		
370	375	380
Met Pro Thr Met Ser Ile Phe Leu Gly Met Ser Tyr Lys Phe Phe Cys		
385	390	395 400
Ala Val Arg Thr Met Tyr Gln		
405		

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 <212> DNA
 <213> Drosophila melanogaster

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<223> DORLU 13.1

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1 5 10 15	
cga gtg cca gta cag ttt tac aga acg att gga gag gat atc tac gcc	96
Arg Val Pro Val Gln Phe Tyr Arg Thr Ile Gly Glu Asp Ile Tyr Ala	
20 25 30	
cat cga tcc acg aat ccc cta aaa tcg ctt ctc ttc aag atc tat cta	144
His Arg Ser Thr Asn Pro Leu Lys Ser Leu Leu Phe Lys Ile Tyr Leu	
35 40 45	
tat gcg gga ttc ata aat ttt aat ctg ttg gta atc ggt gaa ctg gtg	192
Tyr Ala Gly Phe Ile Asn Phe Asn Leu Leu Val Ile Gly Glu Leu Val	
50 55 60	
ttc ttc tac aac tca att cag gac ttt gaa acc att cga ttg gcc atc	240
Phe Phe Tyr Asn Ser Ile Gln Asp Phe Glu Thr Ile Arg Leu Ala Ile	
65 70 75 80	
gcg gtg gct cca tgt atc gga ttt tct ctg gtt gct gat ttt aaa caa	288
Ala Val Ala Pro Cys Ile Gly Phe Ser Leu Val Ala Asp Phe Lys Gln	
85 90 95	
gct gcc atg att aga ggc aag aaa aca cta att atg cta ctc gat gat	336
Ala Ala Met Ile Arg Gly Lys Lys Thr Leu Ile Met Leu Leu Asp Asp	
100 105 110	
ttg gag aac atg cat ccg aaa acc ctg gca aag caa atg gaa tac aaa	384
Leu Glu Asn Met His Pro Lys Thr Leu Ala Lys Gln Met Glu Tyr Lys	
115 120 125	
ttg ccg gac ttt gaa aag acc atg aaa cgt gtg atc aat ata ttc acc	432
Leu Pro Asp Phe Glu Lys Thr Met Lys Arg Val Ile Asn Ile Phe Thr	
130 135 140	
ttt ctc tgc ttg gcc tat acg act acg ttc tcc ttt tat ccg gcc atc	480
Phe Leu Cys Leu Ala Tyr Thr Thr Thr Phe Ser Phe Tyr Pro Ala Ile	
145 150 155 160	
aag gca tcc gtg aaa ttt aat ttc ttg ggc tac gac acc ttt gat cga	528
Lys Ala Ser Val Lys Phe Asn Phe Leu Gly Tyr Asp Thr Phe Asp Arg	
165 170 175	
aat ttt ggt ttc ctc atc tgg ttt ccc ttc gat gca aca agg aat aat	576

Asn	Phe	Gly	Phe	Leu	Ile	Trp	Phe	Pro	Phe	Asp	Ala	Thr	Arg	Asn	Asn		
			180					185						190			
ttg	ata	tac	tgg	atc	atg	tac	tgg	gac	ata	gcc	cat	ggg	gcc	tat	cta	624	
Leu	Ile	Tyr	Trp	Ile	Met	Tyr	Trp	Asp	Ile	Ala	His	Gly	Ala	Tyr	Leu		
		195					200					205					
gcg	ggt	att	gct	ttt	ctc	tgc	gcc	gat	ctt	ttg	ctc	gtc	gta	gtc	att	672	
Ala	Gly	Ile	Ala	Phe	Leu	Cys	Ala	Asp	Leu	Leu	Leu	Val	Val	Val	Ile		
	210					215					220						
acc	cag	att	tgt	atg	cac	ttt	aac	tat	ata	tct	atg	cga	tta	gag	gat	720	
Thr	Gln	Ile	Cys	Met	His	Phe	Asn	Tyr	Ile	Ser	Met	Arg	Leu	Glu	Asp		
225					230					235					240		
cat	cca	tgt	aat	tcg	aat	gag	gac	aaa	gag	aat	ata	gag	ttt	ctt	att	768	
His	Pro	Cys	Asn	Ser	Asn	Glu	Asp	Lys	Glu	Asn	Ile	Glu	Phe	Leu	Ile		
			245					250						255			
ggc	att	atc	aga	tac	cat	gac	aag	tgc	ctt	aaa	cta	tgc	gaa	cat	gtc	816	
Gly	Ile	Ile	Arg	Tyr	His	Asp	Lys	Cys	Leu	Lys	Leu	Cys	Glu	His	Val		
		260					265					270					
aac	gat	ctg	tat	agt	ttc	tct	ttg	ctg	ctt	aat	ttc	ctt	atg	gca	tcc	864	
Asn	Asp	Leu	Tyr	Ser	Phe	Ser	Leu	Leu	Leu	Asn	Phe	Leu	Met	Ala	Ser		
		275					280					285					
atg	cag	att	tgt	ttc	ata	gcc	ttt	cag	gtc	acc	gaa	tca	aca	gtg	gaa	912	
Met	Gln	Ile	Cys	Phe	Ile	Ala	Phe	Gln	Val	Thr	Glu	Ser	Thr	Val	Glu		
	290					295					300						
gtg	att	att	att	tac	tgc	att	ttt	ttg	atg	acc	tcg	atg	gtt	cag	gta	960	
Val	Ile	Ile	Ile	Tyr	Cys	Ile	Phe	Leu	Met	Thr	Ser	Met	Val	Gln	Val		
305				310						315				320			
ttt	atg	gtg	tgc	tac	tat	ggg	gat	act	tta	att	gcc	gcg	agc	ttg	aaa	1008	
Phe	Met	Val	Cys	Tyr	Tyr	Gly	Asp	Thr	Leu	Ile	Ala	Ala	Ser	Leu	Lys		
			325					330					335				
gtg	ggc	gat	gcc	gct	tac	aac	caa	aag	tgg	ttt	cag	tgc	agc	aaa	tcc	1056	
Val	Gly	Asp	Ala	Ala	Tyr	Asn	Gln	Lys	Trp	Phe	Gln	Cys	Ser	Lys	Ser		
		340					345					350					
tat	tgc	acc	atg	ttg	aag	ttg	cta	atc	atg	agg	agt	cag	aaa	cca	gct	1104	
Tyr	Cys	Thr	Met	Leu	Lys	Leu	Leu	Ile	Met	Arg	Ser	Gln	Lys	Pro	Ala		
	355					360					365						
tca	ata	aga	ccg	ccg	act	ttt	ccc	ccc	ata	tcc	ttg	gtt	acc	tat	atg	1152	

Ser Ile Arg Pro Pro Thr Phe Pro Pro Ile Ser Leu Val Thr Tyr Met
 370 375 380

aag gtc atc agc atg tcg tat caa ttt ttt gcc tta ctt aga acc aca 1200
 Lys Val Ile Ser Met Ser Tyr Gln Phe Phe Ala Leu Leu Arg Thr Thr
 385 390 395 400

tac agc aat aat 1212
 Tyr Ser Asn Asn

<210> 80
 <211> 404
 <212> PRT
 <213> Drosophila melanogaster

<400> 80
 Met Glu Thr Ala Lys Asp Asn Thr Ala Arg Thr Phe Met Glu Leu Met
 1 5 10 15

Arg Val Pro Val Gln Phe Tyr Arg Thr Ile Gly Glu Asp Ile Tyr Ala
 20 25 30

His Arg Ser Thr Asn Pro Leu Lys Ser Leu Leu Phe Lys Ile Tyr Leu
 35 40 45

Tyr Ala Gly Phe Ile Asn Phe Asn Leu Leu Val Ile Gly Glu Leu Val
 50 55 60

Phe Phe Tyr Asn Ser Ile Gln Asp Phe Glu Thr Ile Arg Leu Ala Ile
 65 70 75 80

Ala Val Ala Pro Cys Ile Gly Phe Ser Leu Val Ala Asp Phe Lys Gln
 85 90 95

Ala Ala Met Ile Arg Gly Lys Lys Thr Leu Ile Met Leu Leu Asp Asp
 100 105 110

Leu Glu Asn Met His Pro Lys Thr Leu Ala Lys Gln Met Glu Tyr Lys
 115 120 125

Leu Pro Asp Phe Glu Lys Thr Met Lys Arg Val Ile Asn Ile Phe Thr
 130 135 140

Phe Leu Cys Leu Ala Tyr Thr Thr Thr Phe Ser Phe Tyr Pro Ala Ile
 145 150 155 160

Lys Ala Ser Val Lys Phe Asn Phe Leu Gly Tyr Asp Thr Phe Asp Arg

175

Tyr Ser Asn Asn

162

233

<210> 81
 <211> 1179
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1179)
 <223> DORLU 14.1

<400> 81
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 Met Glu Pro Val Gln Tyr Ser Tyr Glu Asp Phe Ala Arg Leu Pro Thr
 1 5 10 15
 acg gtg ttc tgg atc atg ggc tac gac atg ctg ggc gtt ccg aag acc 96
 Thr Val Phe Trp Ile Met Gly Tyr Asp Met Leu Gly Val Pro Lys Thr
 20 25 30
 cgc tct cgc agg ata cta tac tgg ata tat cgt ttc ctc tgt ctc gcc 144
 Arg Ser Arg Arg Ile Leu Tyr Trp Ile Tyr Arg Phe Leu Cys Leu Ala
 35 40 45
 agc cat ggg gtc tgt gta gga gtc atg gta ttt cgt atg gtg gag gca 192
 Ser His Gly Val Cys Val Gly Val Met Val Phe Arg Met Val Glu Ala
 50 55 60
 aag acc att gac aat gtt tcg ctg atc atg cgg tat gcc act ctg gtc 240
 Lys Thr Ile Asp Asn Val Ser Leu Ile Met Arg Tyr Ala Thr Leu Val
 65 70 75 80
 acc tat atc atc aac tcg gat acg aaa ttc gca act gtc tta caa agg 288
 Thr Tyr Ile Ile Asn Ser Asp Thr Lys Phe Ala Thr Val Leu Gln Arg
 85 90 95
 agt gca att caa agt cta aac tca aaa ctg gcc gaa cta tat ccg aag 336
 Ser Ala Ile Gln Ser Leu Asn Ser Lys Leu Ala Glu Leu Tyr Pro Lys
 100 105 110
 acc acg ctg gac agg atc tat cac cgg gtg aat gat cac tat tgg acc 384
 Thr Thr Leu Asp Arg Ile Tyr His Arg Val Asn Asp His Tyr Trp Thr
 115 120 125
 aag tca ttt gta tat ttg gtt att atc tac att ggt tcg tcg att atg 432
 Lys Ser Phe Val Tyr Leu Val Ile Ile Tyr Ile Gly Ser Ser Ile Met
 130 135 140

ttt cac gat gct tct ata gcg tac aag agg tac ctg ctc ata atc att 1056
 Phe His Asp Ala Ser Ile Ala Tyr Lys Arg Tyr Leu Leu Ile Ile Ile
 340 345 350

 atc agg gcg cag cag ccc gtg gaa ctt aat gcc atg ggc tac ctg tcc 1104
 Ile Arg Ala Gln Gln Pro Val Glu Leu Asn Ala Met Gly Tyr Leu Ser
 355 360 365

 att tcg ctg gac acc ttt aaa cag ctg atg agc gtc tcc tac cgg gtt 1152
 Ile Ser Leu Asp Thr Phe Lys Gln Leu Met Ser Val Ser Tyr Arg Val
 370 375 380

 ata acc atg ctc atg cag atg att cag 1179
 Ile Thr Met Leu Met Gln Met Ile Gln
 385 390

<210> 82
 <211> 393
 <212> PRT
 <213> Drosophila melanogaster

<400> 82
 Met Glu Pro Val Gln Tyr Ser Tyr Glu Asp Phe Ala Arg Leu Pro Thr
 1 5 10 15

 Thr Val Phe Trp Ile Met Gly Tyr Asp Met Leu Gly Val Pro Lys Thr
 20 25 30

 Arg Ser Arg Arg Ile Leu Tyr Trp Ile Tyr Arg Phe Leu Cys Leu Ala
 35 40 45

 Ser His Gly Val Cys Val Gly Val Met Val Phe Arg Met Val Glu Ala
 50 55 60

 Lys Thr Ile Asp Asn Val Ser Leu Ile Met Arg Tyr Ala Thr Leu Val
 65 70 75 80

 Thr Tyr Ile Ile Asn Ser Asp Thr Lys Phe Ala Thr Val Leu Gln Arg
 85 90 95

 Ser Ala Ile Gln Ser Leu Asn Ser Lys Leu Ala Glu Leu Tyr Pro Lys
 100 105 110

 Thr Thr Leu Asp Arg Ile Tyr His Arg Val Asn Asp His Tyr Trp Thr
 115 120 125

 Lys Ser Phe Val Tyr Leu Val Ile Ile Tyr Ile Gly Ser Ser Ile Met

165

140

Ile Thr Met Leu Met Gln Met Ile Gln

166

237

385

390

<210> 83

<211> 1134

<212> DNA

<213> *Drosophila melanogaster*

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<221> CDS

<222> (1)..(1134)

<223> DORLU 15.1

<400> 83

atg	gac	gcc	agc	tac	ttt	gcc	gtc	cag	aga	aga	gct	ctg	gaa	ata	gtt	48
Met	Asp	Ala	Ser	Tyr	Phe	Ala	Val	Gln	Arg	Arg	Ala	Leu	Glu	Ile	Val	
1				5				10					15			

gga	ttc	gat	ccc	agt	act	ccg	caa	ctg	agt	ctg	aaa	cat	ccc	atc	tgg	96
Gly	Phe	Asp	Pro	Ser	Thr	Pro	Gln	Leu	Ser	Leu	Lys	His	Pro	Ile	Trp	
			20					25					30			

gcc	ggg	att	ctc	atc	ctg	tcc	ttg	atc	tct	cac	aac	tgg	ccc	atg	gta	144
Ala	Gly	Ile	Leu	Ile	Leu	Ser	Leu	Ile	Ser	His	Asn	Trp	Pro	Met	Val	
		35					40					45				

gtc	tat	gcc	ctg	cag	gat	ctc	tcc	gac	ttg	acc	cgt	ctg	acg	gac	aac	192
Val	Tyr	Ala	Leu	Gln	Asp	Leu	Ser	Asp	Leu	Thr	Arg	Leu	Thr	Asp	Asn	
	50					55					60					

ttt	gcg	gtg	ttt	atg	caa	gga	tca	cag	agc	acc	ttc	aag	ttc	ctg	gtc	240
Phe	Ala	Val	Phe	Met	Gln	Gly	Ser	Gln	Ser	Thr	Phe	Lys	Phe	Leu	Val	
65					70					75				80		

atg	atg	gcg	aaa	cga	agg	cgc	att	gga	tcg	ttg	att	cac	cgt	ttg	cat	288
Met	Met	Ala	Lys	Arg	Arg	Arg	Ile	Gly	Ser	Leu	Ile	His	Arg	Leu	His	
				85				90						95		

aag	cta	aac	cag	gcg	gcc	agt	gcc	acg	ccc	aat	cac	ctg	gag	aag	atc	336
Lys	Leu	Asn	Gln	Ala	Ala	Ser	Ala	Thr	Pro	Asn	His	Leu	Glu	Lys	Ile	
			100					105					110			

gag	agg	gaa	aac	caa	ctg	gat	agg	tat	gtc	gcc	agg	tcc	ttt	aga	aat	384
Glu	Arg	Glu	Asn	Gln	Leu	Asp	Arg	Tyr	Val	Ala	Arg	Ser	Phe	Arg	Asn	
		115					120					125				

gcc	gcc	tac	gga	gtg	att	tgt	gcc	tcg	gcc	ata	gcg	ccc	atg	ttg	ctt	432
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167

238

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 <212> DNA
 <213> Drosophila melanogaster

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 <222> (1)..(1065)
 <223> DORLU 16.1

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 Met Glu Lys Leu Arg Ser Tyr Glu Asp Phe Ile Phe Met Ala Asn Met
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atg ttc aag acc ctt ggc tac gat cta ttc cat aca ccc aaa ccc tgg 96
 Met Phe Lys Thr Leu Gly Tyr Asp Leu Phe His Thr Pro Lys Pro Trp
 20 25 30

tgg cgc tat ctg ctt gtg cga gga tac ttc gtt ttg tgc acg atc agc 144
 Trp Arg Tyr Leu Leu Val Arg Gly Tyr Phe Val Leu Cys Thr Ile Ser
 35 40 45

aac ttt tac gag gct tcc atg gtg acg aca agg ata att gag tgg gaa 192
 Asn Phe Tyr Glu Ala Ser Met Val Thr Thr Arg Ile Ile Glu Trp Glu
 50 55 60

tcc ttg gcc gga agt ccc tcc aaa ata atg cga cag ggt ctg cac ttc 240
 Ser Leu Ala Gly Ser Pro Ser Lys Ile Met Arg Gln Gly Leu His Phe
 65 70 75 80

ttt tac atg ttg agt agc caa ttg aaa ttt atc aca ttc atg ata aat 288
 Phe Tyr Met Leu Ser Ser Gln Leu Lys Phe Ile Thr Phe Met Ile Asn
 85 90 95

cgc aaa cgc cta ctg cag ctg agc cat cgt ttg aaa gag ttg tat cct 336
 Arg Lys Arg Leu Leu Gln Leu Ser His Arg Leu Lys Glu Leu Tyr Pro
 100 105 110

cat aaa gag caa aat caa agg aag tac gag gtg aat aaa tac tac cta 384
 His Lys Glu Gln Asn Gln Arg Lys Tyr Glu Val Asn Lys Tyr Tyr Leu
 115 120 125

tcc tgt tcc acg cgc aat gtt ttg tac gtg tac tac ttt gta atg gtc 432
 Ser Cys Ser Thr Arg Asn Val Leu Tyr Val Tyr Phe Val Met Val
 130 135 140

gtc atg gca ctg gaa ccc ctc gtt cag tcg tgc att atc cag ttc ata 480

Ile Leu Met Thr Ile Thr Tyr Arg Phe Phe Ala Val Ile Arg Gln Thr
 340 345 350

gta gaa aag
 Val Glu Lys
 355

1065

<210> 86
 <211> 355
 <212> PRT
 <213> Drosophila melanogaster

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 Met Glu Lys Leu Arg Ser Tyr Glu Asp Phe Ile Phe Met Ala Asn Met
 1 5 10 15

Met Phe Lys Thr Leu Gly Tyr Asp Leu Phe His Thr Pro Lys Pro Trp
 20 25 30

Trp Arg Tyr Leu Leu Val Arg Gly Tyr Phe Val Leu Cys Thr Ile Ser
 35 40 45

Asn Phe Tyr Glu Ala Ser Met Val Thr Thr Arg Ile Ile Glu Trp Glu
 50 55 60

Ser Leu Ala Gly Ser Pro Ser Lys Ile Met Arg Gln Gly Leu His Phe
 65 70 75 80

Phe Tyr Met Leu Ser Ser Gln Leu Lys Phe Ile Thr Phe Met Ile Asn
 85 90 95

Arg Lys Arg Leu Leu Gln Leu Ser His Arg Leu Lys Glu Leu Tyr Pro
 100 105 110

His Lys Glu Gln Asn Gln Arg Lys Tyr Glu Val Asn Lys Tyr Tyr Leu
 115 120 125

Ser Cys Ser Thr Arg Asn Val Leu Tyr Val Tyr Tyr Phe Val Met Val
 130 135 140

Val Met Ala Leu Glu Pro Leu Val Gln Ser Cys Ile Ile Gln Phe Ile
 145 150 155 160

Val Asn Val Ser Leu Gly Thr Asp Leu Trp Met Met Cys Val Ser Ser
 165 170 175

Gln Ile Ser Met His Leu Gly Tyr Leu Ala Asn Met Leu Ala Ser Ile

173

244

190

Val Glu Lys
355

<400> 87

aac tac atc att tcc tat ttc tgg aat gtg tgt gct gca ttg ggc gtg	624
Asn Tyr Ile Ile Ser Tyr Phe Trp Asn Val Cys Ala Ala Leu Gly Val	
195 200 205	
gca ctg ccc acc gtt tgt gtg gac aca ctg ttc tgt tct ctg agc cat	672
Ala Leu Pro Thr Val Cys Val Asp Thr Leu Phe Cys Ser Leu Ser His	
210 215 220	
aat ctc tgt gcc cta ttc cag att gcc agg cac aaa atg atg cac ttt	720
Asn Leu Cys Ala Leu Phe Gln Ile Ala Arg His Lys Met Met His Phe	
225 230 235 240	
gag ggc aga aat acc aaa gag act cat gag aac tta aag cac gtg ttt	768
Glu Gly Arg Asn Thr Lys Glu Thr His Glu Asn Leu Lys His Val Phe	
245 250 255	
caa cta tat gcg ttg tgt ttg aac ctg ggc cat ttc tta aac gaa tat	816
Gln Leu Tyr Ala Leu Cys Leu Asn Leu Gly His Phe Leu Asn Glu Tyr	
260 265 270	
ttc aga ccg ctc atc tgc cag ttt gtg gca gcc tca ctg cac ttg tgt	864
Phe Arg Pro Leu Ile Cys Gln Phe Val Ala Ala Ser Leu His Leu Cys	
275 280 285	
gtc ctg tgc tac caa ctg tct gcc aat atc ctg cag cca gcg tta ctc	912
Val Leu Cys Tyr Gln Leu Ser Ala Asn Ile Leu Gln Pro Ala Leu Leu	
290 295 300	
ttc tat gcc gca ttt acg gca gca gtt gtt ggc cag gtg tct ata tac	960
Phe Tyr Ala Ala Phe Thr Ala Ala Val Val Gly Gln Val Ser Ile Tyr	
305 310 315 320	
tgc ttc tgc gga tgc agc atc cat tgc gag tgt cag cta ttt ggc cag	1008
Cys Phe Cys Gly Ser Ser Ile His Ser Glu Cys Gln Leu Phe Gly Gln	
325 330 335	
gcc atc tac gag tcc agc tgg ccc cat ctg ctg cag gaa aac ctg cag	1056
Ala Ile Tyr Glu Ser Ser Trp Pro His Leu Leu Gln Glu Asn Leu Gln	
340 345 350	
ctt gta agc tcc tta aaa att gcc atg atg cga tgc agt ttg gga tgt	1104
Leu Val Ser Ser Leu Lys Ile Ala Met Met Arg Ser Ser Leu Gly Cys	
355 360 365	
ccc atc gat ggt tac ttc ttc gag gcc aat cgg gag acg ctc atc acg	1152
Pro Ile Asp Gly Tyr Phe Phe Glu Ala Asn Arg Glu Thr Leu Ile Thr	
370 375 380	

atc cct ggc cta gct ttc cgg gct ttc att att cag tgg ttc agt cgt 1200
 Ile Pro Gly Leu Ala Phe Arg Ala Phe Ile Ile Gln Trp Phe Ser Arg
 385 390 395 400

tcg ggt ttg ttt aac tcc gga aat att tac aat tat gct tta agc cgg 1248
 Ser Gly Leu Phe Asn Ser Gly Asn Ile Tyr Asn Tyr Ala Leu Ser Arg
 405 410 415

tgt tgt tac agc cag ttg gct aat 1272
 Cys Cys Tyr Ser Gln Leu Ala Asn
 420

<210> 88

<211> 424

<212> PRT

<213> Drosophila melanogaster

<400> 88

Met Leu Thr Asp Lys Phe Leu Arg Leu Gln Ser Ala Leu Phe Arg Leu
 1 5 10 15

Leu Gly Leu Glu Leu Leu His Glu Gln Asp Val Gly His Arg Tyr Pro
 20 25 30

Trp Arg Ser Ile Cys Cys Ile Leu Ser Val Ala Ser Phe Met Pro Leu
 35 40 45

Thr Ile Ala Phe Gly Leu Gln Asn Val Gln Asn Val Glu Gln Leu Thr
 50 55 60

Asp Ser Leu Cys Ser Val Leu Val Asp Leu Leu Ala Leu Cys Lys Ile
 65 70 75 80

Gly Leu Phe Leu Trp Leu Tyr Lys Asp Phe Lys Phe Leu Ile Gly Gln
 85 90 95

Phe Tyr Cys Val Leu Gln Thr Glu Thr His Thr Ala Val Ala Glu Met
 100 105 110

Ile Val Thr Arg Glu Ser Arg Arg Asp Gln Phe Ile Ser Ala Met Tyr
 115 120 125

Ala Tyr Cys Phe Ile Thr Ala Gly Leu Ser Ala Cys Leu Met Ser Pro
 130 135 140

Leu Ser Met Leu Ile Ser Tyr His Glu Gln Val Asn Cys Ser Arg Asn
 145 150 155 160

Cys Cys Tyr Ser Gln Leu Ala Asn
420

<210> 89
<211> 1176
<212> DNA
<213> Drosophila melanogaster

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<222> (1)..(1176)
<223> DORLU 24.1

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Met Ser Lys Leu Ile Glu Val Phe Leu Gly Asn Leu Trp Thr Gln Arg
1 5 10 15
ttt acc ttc gcc cga atg ggt ttg gat ttg cag ccc gat aaa aag ggc 96
Phe Thr Phe Ala Arg Met Gly Leu Asp Leu Gln Pro Asp Lys Lys Gly
20 25 30
aat gtt ttg cga tct ccg ctt ctt tat tgt att atg tgt ctg aca aca 144
Asn Val Leu Arg Ser Pro Leu Leu Tyr Cys Ile Met Cys Leu Thr Thr
35 40 45
agc ttt gag ctc tgc acc gtg tgc gcc ttt atg gtc caa aat cgc aac 192
Ser Phe Glu Leu Cys Thr Val Cys Ala Phe Met Val Gln Asn Arg Asn
50 55 60
caa atc gtg ctt tgt tcc gag gcc ctg atg cac gga cta cag atg gtc 240
Gln Ile Val Leu Cys Ser Glu Ala Leu Met His Gly Leu Gln Met Val
65 70 75 80
tcc tcg cta ctg aag atg gct ata ttc ttg gcc aaa tct cac gac ctg 288
Ser Ser Leu Leu Lys Met Ala Ile Phe Leu Ala Lys Ser His Asp Leu
85 90 95
gtg gac cta att caa cag att cag tcg cct ttt aca gag gag gat ctt 336
Val Asp Leu Ile Gln Gln Ile Gln Ser Pro Phe Thr Glu Glu Asp Leu
100 105 110
gta ggt aca gag tgg aga tcc caa aat caa agg gga caa cta atg gct 384
Val Gly Thr Glu Trp Arg Ser Gln Asn Gln Arg Gly Gln Leu Met Ala
115 120 125

gcc att tac ttt atg atg tgt gcc ggt acg agt gtg tca ttt ctg ttg	432
Ala Ile Tyr Phe Met Met Cys Ala Gly Thr Ser Val Ser Phe Leu Leu	
130 135 140	
atg cca gtg gct ttg acc atg ctt aag tac cat tcc act ggg gaa ttc	480
Met Pro Val Ala Leu Thr Met Leu Lys Tyr His Ser Thr Gly Glu Phe	
145 150 155 160	
gcg cct gtc agc tcg ttc cgg gtt ctg ctt cca tac gat gtg aca caa	528
Ala Pro Val Ser Ser Phe Arg Val Leu Leu Pro Tyr Asp Val Thr Gln	
165 170 175	
ccg cat gtt tat gcc atg gac tgc tgc ttg atg gta ttt gtg tta agt	576
Pro His Val Tyr Ala Met Asp Cys Cys Leu Met Val Phe Val Leu Ser	
180 185 190	
ttt ttt tgc tgc tcc acc acc gga gtg gat acc tta tat gga tgg tgt	624
Phe Phe Cys Cys Ser Thr Thr Gly Val Asp Thr Leu Tyr Gly Trp Cys	
195 200 205	
gct tta ggc gtg agt tta caa tac cgt cgc ctc ggt caa caa ctt aaa	672
Ala Leu Gly Val Ser Leu Gln Tyr Arg Arg Leu Gly Gln Gln Leu Lys	
210 215 220	
agg ata ccc tcc tgt ttc aat cca tct cgg tct gac ttt gga tta agt	720
Arg Ile Pro Ser Cys Phe Asn Pro Ser Arg Ser Asp Phe Gly Leu Ser	
225 230 235 240	
ggg att ttt gtg gag cat gct cgt ctg ctt aaa ata gtc caa cat ttt	768
Gly Ile Phe Val Glu His Ala Arg Leu Leu Lys Ile Val Gln His Phe	
245 250 255	
aat tat agt ttt atg gag atc gca ttt gtg gag gtt gtt ata atc tgt	816
Asn Tyr Ser Phe Met Glu Ile Ala Phe Val Glu Val Val Ile Ile Cys	
260 265 270	
gga ctc tat tgc tca gta att tgt cag tat ata atg cca cac acc aac	864
Gly Leu Tyr Cys Ser Val Ile Cys Gln Tyr Ile Met Pro His Thr Asn	
275 280 285	
caa aac ttc gcc ttt ctg ggt ttc ttt tca ttg gta gtt acc aca cag	912
Gln Asn Phe Ala Phe Leu Gly Phe Phe Ser Leu Val Val Thr Thr Gln	
290 295 300	
ctg tgc atc tat ctt ttc ggt gcc gaa cag gtc cgt ttg gag gct gag	960
Leu Cys Ile Tyr Leu Phe Gly Ala Glu Gln Val Arg Leu Glu Ala Glu	
305 310 315 320	

Val Trp Ile Phe Arg Thr Ala Gly Ser Phe Thr Thr Leu Met Asn Ala
 370 375 380

Leu Tyr Ala Lys Tyr Glu Thr His
 385 390

<210> 91
 <211> 1359
 <212> DNA
 <213> Drosophila melanogaster

<220>
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 <222> (1)..(1359)
 <223> DORLU 25.1

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 Met Lys Ser Thr Phe Lys Glu Glu Arg Ile Lys Asp Asp Ser Lys Arg
 1 5 10 15
 cgc gac ctg ttt gta ttc gtg agg caa acc atg tgt ata gcg gcc atg 96
 Arg Asp Leu Phe Val Phe Val Arg Gln Thr Met Cys Ile Ala Ala Met
 20 25 30
 tat ccc ttc ggt tac tac gtg aat gga tct gga gtc ctg gcc gtt ctg 144
 Tyr Pro Phe Gly Tyr Tyr Val Asn Gly Ser Gly Val Leu Ala Val Leu
 35 40 45
 gtg cga ttc tgt gac ttg acc tac gag ctc ttt aac tac ttc gtt tcg 192
 Val Arg Phe Cys Asp Leu Thr Tyr Glu Leu Phe Asn Tyr Phe Val Ser
 50 55 60
 gta cac ata gct ggc ctg tac atc tgc acc atc tac atc aac tat ggg 240
 Val His Ile Ala Gly Leu Tyr Ile Cys Thr Ile Tyr Ile Asn Tyr Gly
 65 70 75 80
 caa ggc gat ttg gac ttc ttc gtg aac tgt ttg ata caa acc att att 288
 Gln Gly Asp Leu Asp Phe Phe Val Asn Cys Leu Ile Gln Thr Ile Ile
 85 90 95
 tat ctg tgg aca ata gcg atg aaa ctc tac ttt cgg agg ttc aga cct 336
 Tyr Leu Trp Thr Ile Ala Met Lys Leu Tyr Phe Arg Arg Phe Arg Pro
 100 105 110

15

Gln Ala Glu Gln Ser Ala Ala Asp Val Glu Pro Gly Gln Tyr Ala Tyr

186

257

270

Met Asp Ala Arg Glu
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<222> (1)..(1296)
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<223> DORLU 26.1

<400> 93

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Met	Lys	Val	Gly	Phe	Ala	Thr	Ile	Gly	Tyr	Ile	Lys	Ser	Ile	Pro	Cys	
1				5				10						15		
cag	gat	gtc	gtt	cac	ata	gtt	ata	tcc	atc	atg	tcc	gag	tgg	tta	cgc	96
Gln	Asp	Val	Val	His	Ile	Val	Ile	Ser	Ile	Met	Ser	Glu	Trp	Leu	Arg	
		20						25					30			
ttt	ctg	aaa	cgc	gat	caa	cag	ctg	gat	gtg	tac	ttt	ttt	gca	gtg	ccc	144
Phe	Leu	Lys	Arg	Asp	Gln	Gln	Leu	Asp	Val	Tyr	Phe	Phe	Ala	Val	Pro	
		35					40						45			
cgc	ttg	agt	tta	gac	ata	atg	ggc	tat	tgg	ccg	ggc	aaa	act	ggt	gat	192
Arg	Leu	Ser	Leu	Asp	Ile	Met	Gly	Tyr	Trp	Pro	Gly	Lys	Thr	Gly	Asp	
	50					55					60					
aca	tgg	ccc	tgg	aga	tcc	ctg	att	cac	ttc	gca	atc	ctg	gcc	att	ggc	240
Thr	Trp	Pro	Trp	Arg	Ser	Leu	Ile	His	Phe	Ala	Ile	Leu	Ala	Ile	Gly	
65					70				75						80	
gtg	gcc	acc	gaa	ctg	cat	gct	ggc	atg	tgt	ttt	cta	gac	cga	cag	cag	288
Val	Ala	Thr	Glu	Leu	His	Ala	Gly	Met	Cys	Phe	Leu	Asp	Arg	Gln	Gln	
			85					90						95		
att	acc	ttg	gca	ctg	gag	acc	ctc	tgt	cca	gct	ggc	aca	tcg	gcg	gtc	336
Ile	Thr	Leu	Ala	Leu	Glu	Thr	Leu	Cys	Pro	Ala	Gly	Thr	Ser	Ala	Val	
		100						105					110			
acg	ctg	ctc	aag	atg	ttc	cta	atg	ctg	cgc	ttt	cgt	cag	gat	ctc	tcc	384
Thr	Leu	Leu	Lys	Met	Phe	Leu	Met	Leu	Arg	Phe	Arg	Gln	Asp	Leu	Ser	
	115						120					125				
att	atg	tgg	aac	cgc	ctg	agg	ggc	ctg	ctc	ttc	gat	ccc	aac	tgg	gag	432
Ile	Met	Trp	Asn	Arg	Leu	Arg	Gly	Leu	Leu	Phe	Asp	Pro	Asn	Trp	Glu	
	130					135					140					
cga	ccc	gag	cag	cgg	gac	atc	cgg	cta	aag	cac	tcg	gcc	atg	gcg	gct	480
Arg	Pro	Glu	Gln	Arg	Asp	Ile	Arg	Leu	Lys	His	Ser	Ala	Met	Ala	Ala	
145					150					155				160		
cgc	atc	aat	ttc	tgg	ccc	ctg	tca	gcc	gga	ttc	ttc	aca	tgc	acc	acc	528
Arg	Ile	Asn	Phe	Trp	Pro	Leu	Ser	Ala	Gly	Phe	Phe	Thr	Cys	Thr	Thr	
			165					170					175			
tac	aac	cta	aag	ccg	ata	ctg	atc	gca	atg	ata	ttg	tat	ctc	cag	aat	576

Tyr Asn Leu Lys Pro Ile Leu Ile Ala Met Ile Leu Tyr Leu Gln Asn	
180	185 190
cgt tac gag gac ttc gtt tgg ttt aca ccc ttc aat atg act atg ccc	624
Arg Tyr Glu Asp Phe Val Trp Phe Thr Pro Phe Asn Met Thr Met Pro	
195	200 205
aaa gtt ctg cta aac tat cca ttt ttt ccc ctg acc tac ata ttt att	672
Lys Val Leu Leu Asn Tyr Pro Phe Phe Pro Leu Thr Tyr Ile Phe Ile	
210	215 220
gcc tat acg ggc tat gtg acc atc ttt atg ttc ggc ggc tgt gat ggt	720
Ala Tyr Thr Gly Tyr Val Thr Ile Phe Met Phe Gly Gly Cys Asp Gly	
225	230 235 240
ttt tat ttc gag ttc tgt gcc cac cta tca gct ctt ttc gaa gtg ctc	768
Phe Tyr Phe Glu Phe Cys Ala His Leu Ser Ala Leu Phe Glu Val Leu	
245	250 255
cag gcg gag ata gaa tca atg ttt aga ccc tac act gat cac ttg gaa	816
Gln Ala Glu Ile Glu Ser Met Phe Arg Pro Tyr Thr Asp His Leu Glu	
260	265 270
ctg tcg cca gtg cag ctt tac att tta gag caa aag atg cga tca gta	864
Leu Ser Pro Val Gln Leu Tyr Ile Leu Glu Gln Lys Met Arg Ser Val	
275	280 285
atc att agg cac aat gcc atc atc gat ttg acc aga ttt ttt cgt gat	912
Ile Ile Arg His Asn Ala Ile Ile Asp Leu Thr Arg Phe Phe Arg Asp	
290	295 300
cgc tat acc att att acc ctg gcc cat ttt gtg tcc gcc gcc atg gtg	960
Arg Tyr Thr Ile Ile Thr Leu Ala His Phe Val Ser Ala Ala Met Val	
305	310 315 320
att gga ttc agc atg gtt aat ctc ctg aca ttg ggc aat aat ggt ctg	1008
Ile Gly Phe Ser Met Val Asn Leu Leu Thr Leu Gly Asn Asn Gly Leu	
325	330 335
ggc gca atg ctc tat gtg gcc tac acg gtt gcc gct ttg agc caa ctg	1056
Gly Ala Met Leu Tyr Val Ala Tyr Thr Val Ala Ala Leu Ser Gln Leu	
340	345 350
ctg gtt tat tgc tat ggc gga act ctg gtg gcc gaa agt agc act ggt	1104
Leu Val Tyr Cys Tyr Gly Gly Thr Leu Val Ala Glu Ser Ser Thr Gly	
355	360 365
ctg tgc cga gcc atg ttc tcc tgt ccg tgg cag ctt ttt aag cct aaa	1152

Arg Pro Glu Gln Arg Asp Ile Arg Leu Lys His Ser Ala Met Ala Ala
145 150 155 160

Arg Ile Asn Phe Trp Pro Leu Ser Ala Gly Phe Phe Thr Cys Thr Thr
165 170 175

Tyr Asn Leu Lys Pro Ile Leu Ile Ala Met Ile Leu Tyr Leu Gln Asn
180 185 190

Arg Tyr Glu Asp Phe Val Trp Phe Thr Pro Phe Asn Met Thr Met Pro
195 200 205

Lys Val Leu Leu Asn Tyr Pro Phe Phe Pro Leu Thr Tyr Ile Phe Ile
210 215 220

Ala Tyr Thr Gly Tyr Val Thr Ile Phe Met Phe Gly Gly Cys Asp Gly
225 230 235 240

Phe Tyr Phe Glu Phe Cys Ala His Leu Ser Ala Leu Phe Glu Val Leu
245 250 255

Gln Ala Glu Ile Glu Ser Met Phe Arg Pro Tyr Thr Asp His Leu Glu
260 265 270

Leu Ser Pro Val Gln Leu Tyr Ile Leu Glu Gln Lys Met Arg Ser Val
275 280 285

Ile Ile Arg His Asn Ala Ile Ile Asp Leu Thr Arg Phe Phe Arg Asp
290 295 300

Arg Tyr Thr Ile Ile Thr Leu Ala His Phe Val Ser Ala Ala Met Val
305 310 315 320

Ile Gly Phe Ser Met Val Asn Leu Leu Thr Leu Gly Asn Asn Gly Leu
325 330 335

Gly Ala Met Leu Tyr Val Ala Tyr Thr Val Ala Ala Leu Ser Gln Leu
340 345 350

Leu Val Tyr Cys Tyr Gly Gly Thr Leu Val Ala Glu Ser Ser Thr Gly
355 360 365

Leu Cys Arg Ala Met Phe Ser Cys Pro Trp Gln Leu Phe Lys Pro Lys
370 375 380

Gln Arg Arg Leu Val Gln Leu Leu Ile Leu Arg Ser Gln Arg Pro Val
385 390 395 400

Ser Met Ala Val Pro Phe Phe Ser Pro Ser Leu Ala Thr Phe Ala Ala
 405 410 415

Ile Leu Gln Thr Ser Gly Ser Ile Ile Ala Leu Val Lys Ser Phe Gln
 420 425 430

<210> 95
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 <212> DNA
 <213> Drosophila melanogaster

<220>
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 <223> DORLU 27.1

<400> 95
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 Leu Leu Pro Tyr Arg Ser Lys Trp His Thr Leu Val Tyr Ile Gln Met
 20 25 30
 gtt ata ttt ttt gct tca atg agc ttt ggc tta acg gaa tcg atg gga 144
 Val Ile Phe Phe Ala Ser Met Ser Phe Gly Leu Thr Glu Ser Met Gly
 35 40 45
 gac cat gtt caa atg gga cgg gac tta gcc ttc atc ctt ggg aca tat 192
 Asp His Val Gln Met Gly Arg Asp Leu Ala Phe Ile Leu Gly Thr Tyr
 50 55 60
 tat ttc tgc tgg tat ggc gat gaa ctt gac caa gtg atc agc gat ctg 240
 Tyr Phe Cys Trp Tyr Gly Asp Glu Leu Asp Gln Val Ile Ser Asp Leu
 65 70 75 80
 gac gct cta cat cct tgg gca cag aaa ggt cct aat cca gtt gaa tat 288
 Asp Ala Leu His Pro Trp Ala Gln Lys Gly Pro Asn Pro Val Glu Tyr
 85 90 95
 cag act ggt aaa cgt tgg tac ttc gta atg gct ttt ttc ttg gca acg 336
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Asp His Val Gln Met Gly Arg Asp Leu Ala Phe Ile Leu Gly Thr Tyr
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Tyr Phe Cys Trp Tyr Gly Asp Glu Leu Asp Gln Val Ile Ser Asp Leu
 65 70 75 80

Asp Ala Leu His Pro Trp Ala Gln Lys Gly Pro Asn Pro Val Glu Tyr
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Gln Thr Gly Lys Arg Trp Tyr Phe Val Met Ala Phe Phe Leu Ala Thr
 100 105 110

Ser Trp Ser Phe Phe Leu Cys Ile Leu Leu Leu Leu Ile Thr Ser
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Pro Met Trp Val His Gln Gln Asn Leu Pro Phe His Ala Ala Phe Pro
 130 135 140

Phe Gln Trp His Glu Lys Ser Leu His Pro Ile Ser His Ala Ile Ile
 145 150 155 160

Tyr Leu Phe Gln Ser Tyr Phe Ala Val Tyr Cys Leu Thr Trp Leu Leu
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 Cys Ile Glu Gly Leu Ser Ile Cys Ile Tyr Ala Glu Ile Thr Phe Gly
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 Ile Glu Val Leu Cys Leu Glu Leu Arg Gln Ile His Arg His Asn Tyr
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 Gly Leu Gln Glu Leu Arg Met Glu Thr Asn Arg Leu Val Lys Leu His
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 Gln Lys Ile Met Gly Val Asn Phe Ser Leu Val Ser Leu Ser Val Leu
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 Val Leu Met Leu Leu Ala Leu Gly His Leu Ser Met Trp Ser Tyr Cys
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 Glu Ala Tyr Asp Pro Thr Lys Gly Ser Lys Asp Val Tyr Arg Asp Leu
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 Cys Val Ile Ile Arg Arg Gly Gln Asp Pro Leu Ile Met Arg Ala Ser
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Tyr Val Asp Ile Tyr Leu Ser Thr Glu Ser Leu Asp Phe Ile Ile Arg
50 55 60

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Asn Val Tyr Leu Ala Val Leu Phe Thr Asn Thr Val Val Arg Gly Val
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Leu Leu Cys Val Gln Arg Phe Ser Tyr Glu Arg Phe Ile Asn Ile Leu
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Lys Ser Phe Tyr Ile Glu Leu Leu Gln Ser Asp Asp Pro Ile Ile Asn
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Lys Ser Phe Tyr Ile Glu Leu Leu Gln Ser Asp Asp Pro Ile Ile Asn
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198

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Glu Phe Leu Cys Phe Gly Ala Met Leu Cys Val Leu Leu Phe Ser Leu
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Lys Tyr Gly Ile Leu Gln Ser Phe Asp Ile Ala Ile Ala Ala Tyr Glu
325 330 335

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340 345 350

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 <222> (849)..(1030)

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<212> DNA

<213> *Drosophila melanogaster*

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<222> (1)..(120)

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<222> (852)..(930)

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